

SEQUENCE LISTING

01100 Pompejus, Markus
 Krieger, Burkhard
 Schroder, Hartwig
 Felder, Oskar
 Heberbauer, Gregor
 Kim, Sun-Won
 Lee, Heung-Schick
 Hwang, Byung-Joon



01200 Corynebacterium glutamicum GENES ENCODING
 METABOLIC PATHWAY PROTEINS

01300 BGI-121CP2

01400 13 19,746,660

01410 1400-12-22

01500 18 60,741

01510 1100-6-12

01600 14 60,124

01610 1100-6-13

01700 14 141,081

01710 1100-6-17

01800 14 101

01810 1100-9-25

01900 14 811

01910 1100-6-15

02000 18 971

02010 1100-3-19

02100 19 614,019

02110 1100-7-17

02200 1100

02300 Patent In Vers. 2.0

02400 1

02410 1:40

02420 TGA

02430 Corynebacterium glutamicum

02500

02510 100

02520 (363)(111676)

04000 1

gagaaaatgt gtgagaaaat gcatgcagaa aaaggaaagt tcgggccaaag atgggtgttt 60

ctgtatcagg atgatcggat ctttgacaga tgggtatgag acaaatacacc gagagttgtt 120

aattctaac aatggaaaag taacattgag agatgattta taccatcctg caccatttag 180

agtggggcta gtcatacccc cataacccta gctgtacgca atcagatttca aatcagttgg 240

aaaaagtcaa gaaaattacc cgagaattaa tttataccac acagtctatt gcaatagacc 300
 aaggtgttca gtaggggtgca tgggagaaga atttctaatt aaaaactctt aaggaoctcc 360
 aa atg cca aag tac gac aat tcc aat gct gac cag tgg ggc ttt gaa 407
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu
 1 5 10 15
 acc cgc tcc att cac gca ggc cag tca gta gac gca cag acc agc gca 455
 Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala
 20 25 30
 cga aac ctt cgg acc tac caa tcc acc gct ttc gtg ttc gac tcc gct 503
 Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala
 35 40 45
 gag cac ggc aag cag cgt ttc gca ctt gag gat cta ggc cct gtt tac 551
 Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr
 50 55 60
 tcc cgc ctc acc aac cta acc gtt gag gct ttg gaa aac cgc atc gct 599
 Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala
 65 70 75
 tcc ctc gaa ggt ggc gtc cac gct gta ggc ttc tcc ttc gga cag ggc 647
 Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala
 80 85 90 95
 gca acc acc aac ggc att ttg aac ctg gca ggc ggc ggc gac cag acc 695
 Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile
 100 105 110
 gtc acc tcc cca cgc ctc tac ggt ggc acc gac act cta ttc ctc atc 743
 Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile
 115 120 125
 acc ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg gaa aac ccc gac 791
 Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp
 130 135 140
 gag cct gag ttc tgg tag gca gcc gtt cag cca aac acc aaa gca ttc 839
 Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe
 145 150 155
 ttc ggc gag act ttc gcc aac cca cag gca gac gtc ctg gat att cct 887
 Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro
 160 165 170 175
 cgc gtg gct gaa gtt cgc cac cgc aac agc gtt cca ctg atc atc gac 935
 Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp
 180 185 190
 aac acc atc gct acc gca ggc ctc ctg cgc cgc ctc gag ctc ggc gca 983
 Asn Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala
 195 200 205
 gag gtt gtc gtc gct tcc ctc acc aag ttc ttc acc gcc aac ggc tcc 1031
 Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser
 210 215 220

gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc gat tgg act gtc 1079
 Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val
 215 230 235

gaa aag gat gga aag cca gta ttc ccc tac ttc gtc act cca gat gct 1127
 Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala
 240 245 250 255

gct tac cac gga ttg aag tac gca gat ctt ggt gca cca gcc ttc ggc 1175
 Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly
 260 265 270

ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc ctc tcc 1223
 Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser
 275 280 285

gca tcc aac gca tgg gct gca gtc cag ggc atc gac acc ctt tcc ctg 1271
 Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu
 290 295 300

cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa ttc ctc 1319
 Arg Ile Gln Arg His Asn Glu Asn Ala Ile Lys Val Ala Gln Phe Leu
 305 310 315

aac aac cac gag aag ctg gaa aag gtt aac ttc gca acc ctg aag gat 1367
 Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp
 320 325 330 335

tcc ctt tgg tac gaa acc aag gaa aag ctt gcc ctg aag tac acc gcc 1415
 Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly
 340 345 350

tcc att ctc aac tac aag atc aag gcc ggc aag gat aag gct tgg gca 1463
 Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala
 355 360 365

ttt atc gac ccc ctg aag cta cac ttc aac ctt gca aac atc cgc gat 1511
 Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp
 370 375 380

gtt cgc tcc ctc gtt gtt cac gca gaa acc acc acc cat tca aag tcc 1559
 Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser
 385 390 395

gac gaa gct ggc ctg gca ggc gag ggc att acc cag tcc acc gtc cgc 1607
 Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg
 400 405 410 415

aag tcc gtt ggc atc gag acc att gat gat atc atc gct gac ctc gaa 1655
 Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu
 420 425 430

ggc ggc ttt gct gca atc tag cttttatatag aactaaccca gtgcttaaag 1706
 Gly Gly Phe Ala Ala Ile
 435

cgttgggttt ttctttttca gactgtgag aatgcaaaact aga tagaca gagctgtcca 1756

tatacaactgg acgaagtttt agtcttgtcc accagaacaa ggcgtttatt ttcattgccc 1826

cccctggccc ttca 1840

02100-2
 02110-437
 02120-PET
 02130-Corynebacterium glutamicum

0400-1
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
 1 5 10 15
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
 165 170 175
 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
 180 185 190
 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
 195 200 205
 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
 210 215 220
 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
 225 230 235 240
 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
 245 250 255
 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
 260 265 270
 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
 275 280 285

Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg
 290 295 300

Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
 305 310 315 320

Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
 325 330 335

Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
 340 345 350

Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
 355 360 365

Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val
 370 375 380

Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
 385 390 395 400

Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
 405 410 415

Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly
 420 425 430

Gly Phe Ala Ala Ile
 435

440 - 3

441 - 1495

442 - DNA

443 - *Corynebacterium glutamicum*

444

445 - GDS

446 - (287)...1264)

447 - 3

ataggtttt ctcagcggaa acggttggc taccagcact ttcacccgaa cagcctgcaa 60

gaagtcggac ggctaacagg gctgggattg tctcaactt caattcggg tcttcttag 120

caataggttc gtagaaaagt ttactagcct agagagtatg cgatttctg aactogaaga 180

attgaagaat cgcggacct tgaaatggac cgggtttcca gaagacgtg ttcctttgtg 240

ggttcgggaa agtgattttg gcacctgccc gcagttgaag gaagct atg gca gat 295
 Met Ala Asp
 1

ccc gtt gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg 343
 Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu
 5 10 15

aat gat ggc ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca 391
 Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Tyr Gly Phe Gly Pro
 20 25 30 35

aat ccc gaa agt gtt ttc gcc att ccc gat gtg gtt cgt ggc ctg aag 439
 Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys
 40 45 50

ctt gcc att gag cat ttc acc aag cct ggt tgg gcc atc att gtg ccc 487
 Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro
 55 60 65

ttg cct gca tac ccc cct ttc att gag tgg cct aag gtg act ggt cgt 525
 Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg
 70 75 80

cag gcc atc tac att gat gcc cat gag tac gat ttg aag gaa att gag 583
 Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu
 85 90 95

ang gcc ttc gct gag ggt cgg gga tca cgt ttc ttc tcc att cca ccc 631
 Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His
 100 105 110 115

aac cca ctg gcc acc gtc ttc tcc gaa gag tac acc ccc gag ctc acc 679
 Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr
 120 125 130

cat att gcc gcc aag tac gat gcc ccc atc acc gcc gat gag atc ccc 727
 Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp Glu Ile His
 135 140 145

cag cca ctg gtc tat gaa gcc acc cat gtg gcc gcc ggt ggt tct 775
 Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala Gly Val Ser
 150 155 160

gag aac gct gca aac att tgc atc acc atc acc gca att tct aag gcc 823
 Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala
 165 170 175

tgg aac act gct gat ttg aag tgc gct cag atc ttc ttc agt aat gaa 871
 Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu
 180 185 190 195

acc gat gag aag gcc tgg aag aat ttg tgg gat att acc cgt gac gat 919
 Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr Arg Asp Gly
 200 205 210

gtg tcc atc ctt gga ttg atc gct gcc gag aca gtg tac aac gag gcc 967
 Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr Asn Glu Gly
 215 220 225

gaa gaa ttc ctt gat gag tca att cag att ctc aag gac aac cgt gac 1015
 Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp Asn Arg Asp
 230 235 240

ttc ccc gct gct gaa ctg gaa aag ctt gcc ctg aag gtc tac gca ccc 1063
 Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val Tyr Ala Pro
 245 250 255

gac tcc act tat ttg atg tgg ttg gac ttc cct gcc acc aag atc gaa 1111
 Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr Lys Ile Glu
 260 265 270 275

gag ggg cct tct aaa att ctt cgt gag gag ggt aag gtc atg ctg aat 1159
 Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val Met Leu Asn
 280 285 290

gat ggc gca ggt ttt ggt ggt ttc acc acc tgc gct cgt ctt aat ttt 1207
 Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg Leu Asn Phe
 295 300 305

ggg tgt tcc aga gag acc ctt gag gag ggg ctg cgc cgt atc gcc agc 1255
 Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg Ile Ala Ser
 310 315 320

ctg ttg taa ataataagta aaaagtctgt cctgattact tctttgatgc 1304
 Val Leu
 325

tggttcacat gttcttcgga gctggaaaacc tcattctccc gctgatggtt ggattgtcgg 1364

caggaaacaa ctattacaa gctattcttag gattcttagc aacgagtgtt ctgctccgg 1424

tgctgggat tatcgcggtg ggtctgtcgg gagaatatgt caaggacatg gctctcgtg 1484

ccgtaagat c 1495

210: 4

211: 125

212: 88T

213: Corynebacterium glutamicum

400: 4

Met Ala Asp Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala
 1 5 10 15

Thr Gly Leu Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly
 20 25 30

Phe Gly Pro Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg
 35 40 45

Gly Leu Lys Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile
 50 55 60

Ile Val Pro Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val
 65 70 75 80

Thr Gly Arg Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys
 85 90 95

Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys
 100 105 110

Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg
 115 120 125

Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp
 130 135 140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala
 145 150 155 160

Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
 165 170 175
 Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
 180 185 190
 Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
 195 200 205
 Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
 210 215 220
 Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
 225 230 235 240
 Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
 245 250 255
 Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
 260 265 270
 Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
 275 280 285
 Met Leu Asn Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg
 290 295 300
 Leu Asn Phe Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg
 305 310 315 320
 Ile Ala Ser Val Leu
 325

<210> 1

<211> 1033

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1006)

<400> 5

gtgcggatcg ggtatccgcg ctacacttag aggtgtaga gatcatgagt ttccacgaac 60

tgtaacgcag gattcaccaa tcaatgaaag gtgcaccgac atg agc act gaa gac 115
 Met Ser Thr Glu Asp
 1 5

att gtc gtc gta gca gta gat ggc tgg gac gcc tca aaa caa gct gtt 163
 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
 10 15 20

cgg tgg gct gca aat acc gcc aac aaa cgt ggc att tca ctt cgc ttg 211
 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
 25 30 35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259
 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
 40 45 50

cca cca caa gag att ttc gat gac etc bag gcc gaa gcc ctg gaa aag Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys 55 60 65	307
att aac gaa gcc agt gac atc gcc cat gag gta gag cca gaa atc aag Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys 70 75 80 85	355
atc ggg cac acc atc ggt gaa gcc agt ccc atc gac atg ctg ctg gaa Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu 90 95 100	403
acc tct ccc gat gcc aca atg atc gtc atg ggt tcc agc gga etc ggc Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly 105 110 115	451
gga etc tct gga atg gtc atg gcc tcc gtc tcc ggt gca ggc etc agc Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser 120 125 130	499
cac gca aag tct cca gtc gtt gtt gtc agt gaa gac agc gca gtc aac His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn 135 140 145	547
gaa gac agc aag cac gcc cca gtc gtc gtc ggt gtc cat gcc tcc gaa Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu 150 155 160 165	595
etc tcc cca bag gca acc caa cac gca ttt ggt gaa tct gaa gct agt Val Ser Gln Gln Ala Thr Glu Cys Ala Phe Ala Glu Ala Glu Ala Arg 170 175 180	643
gcc gcc gaa etc gtc gca ttt cac acc tgg atc gac atg bag cca bag Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln 185 190 195	691
gca tca att gca ggt att gca gct gct caa bag bag tgg gat caa gtc Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val 200 205 210	739
gaa agt cag caa acc gac atg ctg atc gaa ccc etc gca cca ctg gtc Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Asn Leu Ala Pro Leu Val 215 220 225	787
gaa aag cac cca agt gta acc gcc aag aag atc atc acc agt gac agc Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg 230 235 240 245	835
cca gtt ctc gca etc gca gaa gca tct gaa aac ggc cag etc cta gtc Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val 250 255 260	883
gtt ggt tcc cat ggt agt gcc aga ttc aag ggc atg etc ctt agc tcc Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser 265 270 275	931
acc tcc cgc gca ctg ctg caa tcc gca ccc tgc cca atg atg atg gtc Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val 280 285 290	979

cgc cca cct gag aag att aag aag tag tttcttttaa gtttcgatgc cccgggtt 1033
 Arg Pro Pro Glu Lys Ile Lys Lys
 295 300

<210> 6
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 6
 Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
 1 5 10 15
 Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
 20 25 30
 Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
 35 40 45
 Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50 55 60
 Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65 70 75 80
 Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
 85 90 95
 Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110
 Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125
 Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140
 Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160
 Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
 165 170 175
 Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
 180 185 190
 Asp Met Glu Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Glu
 195 200 205
 Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220
 Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

02160: 7
 02110: 948
 02120: DNA
 02130: Corynebacterium glutamicum

02200:
 02210: 3763
 02220: (101)...(925)
 02230: PKA02229

04400: 7
 atggtttcaa cagagaccac cgcgtgtctt gggtcgacgc ctctggcgat cccacgcgac 60
 agccttggga gatitttgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115
 Leu Thr Ile Pro Phe
 1 5
 ggc aac ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163
 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
 10 15 20
 att gcg cgc cta gal tta acc cca gaa atg gty gtc ccg ctg ttt gac 211
 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
 25 30 35
 cgc cgc ggc ggg atc ggt gct gat ggt atc ccc ccg ctg gtt aaa gct 259
 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
 40 45 50
 gca gac gta gaa ggc tcc acg gtc gac cca tcc ctg tgg ttc atg gat 307
 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
 55 60 65
 cac cgc aac gcc gat gaa tct tgg gct gaa atg tcc ggc aat ggt gtg 355
 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
 70 75 80 85
 cgc ctg ttc ggc cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403
 Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
 90 95 100
 age ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg 451
 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
 105 110 115
 cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499
 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
 120 125 130
 gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547
 Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala
 135 140 145

ggc ctt ggc gtt gat atg ggt aac cca cac cta gag tgc gtt gtg cgg 595
Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro
150 155 160 165

ggc tta agt gag tgc gct ctt gcc gat atg gaa ctg cgc gca cct acg 643
Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr
170 175 180

ttt gat cag gaa ttc ttc ccc ccc ggt gtg aac gta gaa atc gtc aca 691
Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr
185 190 195

gaa tta gaa gat gac gca gta tgc atg cgc gtg tgg gaa cgc gga gtg 739
Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val
200 205 210

ggc gaa acc cgc tcc tgt ggc aag gga acc gtu gct gaa gag tgt gct 787
Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala
215 220 225

gct tta gct gat gct gga tgc gga gaa ggc acc gct aca gtc tgc gtc 835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val
230 235 240 245

cac cgt ggg aca gta gaa gtc cag atc ttt gac gac gtc tcc aca ctc 883
Pro Arg Gly Glu Val Glu Val Glu Ile Phe Asp Asp Gly Ser Thr Leu
250 255 260

acc ggc ccc acc gct atc atc gca ctc ggt gaa gtc cag atc 925
Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Glu Ile
265 270 275

taagattgcg gatgtgagtt cgg 948

<210> :

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> :

Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile
1 5 10 15

Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val
20 25 30

Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu
35 40 45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser
50 55 60

Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
65 70 75 80

Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly
85 90 95

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
100 105 110

His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
 115 120 125
 Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
 130 135 140
 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
 145 150 155 160
 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
 165 170 175
 Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
 180 185 190
 Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val
 195 200 205
 Thr Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
 210 215 220
 Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
 225 230 235 240
 Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
 245 250 255
 Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
 260 265 270
 Val Gln Ile
 275

0110 - 9
 0111 - 1491
 0112 - DNA
 0113 - *Corynebacterium glutamicum*

0120 -
 0121 - GDS
 0122 - (1010) .. (1463)
 0123 - EXS02970

0400 - 9
 aacccgacaaa acagccgctc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
 ctatttaaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5
 ttc acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct ggc caa goa 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc ggc cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc ggc cag gac aaa atc agc ccc aaa gta tgg gca gct 259

His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gac gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc cag gaa aac tta ggt cac aac aac cct cgt	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80	
tta gtt gag gag acc cag cgc caa gaa tcc cgt ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
cag gcc ttc ggc aat gat gtg ctc tct tat ggt got gca aag atc gtc	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
cag atg ggc cgt ggc gaa ttc tcc cac atg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc cac ggc atc gag cac tcc atc cgc atg ggt cgc ctg cac acc ggc	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac ala att ctg tcc gca tcc cgc cgc tcc cac ggc gca acc ggc	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160	
tcc cgc acc atg atg ctg acc ggc caa cac cgc tcc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
165 170 175	
acc cac caa gat atc tac cac ttc tgg caa cca ttc ctt cac caa tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
180 185 190	
tcc ttc ttt gcc acc acc caa gaa gaa caa tcc gaa cgc gca ctc aac	739
Ser Phe Phe Ala Thr Thr Gln Gln Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcc ttt gaa ggt got ggc atg atc gca ggc	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtc gtc gga tca tca gaa atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240	
gca cgt tac tta aat gcc gtc cgc gaa ctt tcc aac aag cac gcc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
245 250 255	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aac	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt got tac gag cat got gcc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	

280 285 290
 acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctg ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 305 300 305
 gtg atg acc caa tca atc cgc cat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Gln Ala Tyr Ser
 310 315 320 325
 ggc gga ctg acc tac tcc gga cac cca att gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340
 gca agc atg gag att tac ggc gaa gga gag atc att cca cga gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355
 aga att agc cat gaa ctg atc gaa cat cgc att cgt gaa cta ggc gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370
 gaa aac ctg gag atc gct gac gtc ggc ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
 atg gag ttc aac gcc gac gcc act gcc atg gct gcc gct gct gcc gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405
 ttc gag ttc ctg ggc gtc ggc cgc atg atc tcc ggc aac cga ttc cac 1363
 Phe Lys Ser Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420
 ttc ggc cat ctg ctc acc acc act gat gac gaa ttg gta gca ctg ctg 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asn Glu Leu Val Ala Leu Leu
 425 430 435
 gac cgc gtc gaa gcc gca gcc caa gct gtc gag ctg acc ttc gct ggc 1469
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450
 ggc atg ttc taagttttct agataacaag gcc 1491
 Ala Leu Phe
 455

C110 - 10

C111 - 456

C112 - PRT

C113 - *Corynebacterium glutamicum*

C400 - 10

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Gly Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
370						375					380				
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
385					390					395					400
Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser
				405					410					415	
Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu
			420					425					430		
Leu	Val	Ala	Leu	Leu	Asp	Ala	Val	Glu	Ala	Ala	Ala	Gln	Ala	Val	Glu
			435				440					445			
Leu	Thr	Phe	Ala	Gly	Ala	Leu	Phe								
			450			455									

C.10 - 11

C.11 - 1330

C.12 - DNA

C.13 - Corynebacterium glutamicum

C.20 -

C.21 - CDS

C.22 - 1010... 1330

C.23 - FRXA01019

C.00 - 11

accacacaa accagcgttc acgtgcataa gcagctcggc ttgatctagg gtgaggtgag	60
ttattaaa accatcataat attttgggga gtagaactgt ttg gaa ttg aag ggt	115
	Leu Ala Leu Lys Gly
	1
tac acc aac tit gac ggt gaa ttc atc gaa ttc gga tct gtg caa gaa	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
	10 15 20
aaa aac gag gaa aaa cgg gca ttc gac aac gat cgc ggc cac gtt ttc	211
Lys Gln Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
	25 30 35
cac tcc tgg tcc ggc cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
	40 45 50
gac gaa ggt tcc aag ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Gln Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
	55 60 65
atg ggt tcc caa ctt gtc tgg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
	70 75 80 85
tta gtt gag ggc atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
	90 95 100
cgg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451

Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	Ala	Ala	Lys	Ile	Val	
			105					110					115			
tcc	atg	gac	cgt	ggc	gaa	ttc	tcg	cac	gtg	ttt	ttc	acc	aac	ggc	ggc	499
Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	Phe	Thr	Asn	Gly	Gly	
		120					125				130					
gac	gac	gac	atc	gag	cac	tcg	atc	cgc	atg	gct	cgc	ctg	cac	acc	gga	547
Ala	Asp	Ala	Ile	Gln	His	Ser	Ile	Arg	Met	Ala	Arg	Leu	His	Thr	Gly	
	135					140					145					
cgc	aac	aaa	att	ctg	tcg	gca	tac	cgc	agg	tac	cac	ggc	gca	acc	gga	595
Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	His	Gly	Ala	Thr	Gly	
150					155					160				165		
tcc	gag	atg	atg	ctc	acc	cgc	gaa	cac	cgc	cgc	ctg	ggc	aac	ccc	acc	643
Ser	Ala	Met	Met	Leu	Thr	Gly	Gln	His	Arg	Arg	Leu	Gly	Asn	Pro	Thr	
			170						175					180		
acc	gac	cca	gat	atc	tac	cac	ttc	tgg	gga	cca	ttc	ctg	cac	cac	tcc	691
Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser	
		185						190					195			
tca	ttr	ttr	gac	acc	acc	cac	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aac	739
Ser	Phe	Phe	Ala	Phe	Thr	Gln	Gln	Gln	Gln	Cys	Glu	Arg	Ala	Leu	Lys	
	200						205				210					
cac	ctg	gaa	gat	gtc	atc	cgc	ttr	cac	ggt	gct	ggc	atg	atc	gca	gac	787
His	Leu	Gln	Asp	Val	Ile	Ala	Pro	Gln	Gly	Ala	Gly	Met	Ile	Ala	Ala	
	215					220					225					
atc	gtr	ctg	gag	cca	gtg	ctg	ggt	tcc	cac	gga	atc	atc	ctg	ccc	cca	835
Ile	Val	Leu	Gln	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro	
230					235					240				245		
gca	ggt	tac	tta	aat	ggc	ctg	cgc	gaa	ctt	tgc	aac	aac	cac	ggc	atc	883
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Gln	Leu	Cys	Asn	Lys	His	Gly	Ile	
			250					255					260			
ctc	ttr	atc	gac	gac	gaa	gtc	atg	gtc	gga	tcc	gga	cgc	acc	ggc	aaa	931
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys	
		265						270					275			
ctg	ttr	gct	tac	gag	cat	gct	ggc	gac	gat	tcc	cag	cca	gac	atc	atc	979
Leu	Phe	Ala	Tyr	Gln	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile	
	280						285					290				
acc	ttr	gac	aag	ggt	gtt	aac	gca	ggt	tac	gac	cca	ctc	ggt	ggc	atc	1027
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile	
	295					300					305					
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttr	gga	tca	gag	gca	tac	tcc	1075
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser	
310					315					320				325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gct	aag	1123
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys	
			330						335					340		
gca	gac	ctg	gag	att	tac	gag	gaa	gga	gag	atc	att	cca	cgc	gta	gct	1171
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala	

345	350	355	
gga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta ggc gaa			1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			
360	365	370	
gaa aac gta ggc atc gct gac ggc cgc ggc atc gga ttc ttc tgg gca			1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala			
375	380	385	
tig gag ttc aat gca gac ggc acc ggc atg gct ggc ggt gct gca gaa			1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu			
390	395	400	405
ttc aag gaa cgc ggc			1330
Phe Lys Glu Arg Gly			
410			

0110> 12

0111> 410

0112> PRT

0113> *Corynebacterium glutamicum*

0100> 12

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe			
1	5	10	15
Gly Ser Val Glu Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp			
21	26	31	36
Asn Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro			
38	43	48	
Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly			
51	56	61	
Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly			
65	70	75	80
His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg			
85	90	95	
Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val			
100	105	110	
Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe			
115	120	125	
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala			
130	135	140	
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr			
145	150	155	160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg			
165	170	175	
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro			
180	185	190	

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 His Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

#210 - 13

#211 - 793

#212 - DNA

#213 - *Corynebacterium glutamicum*

#220 -

#221 - CDS

#222 - (101)...(769)

#223 - EXC02390

#400 - 13

gtctgtgtgtg ctgaaccata cgtctggaact ccactctgtg ttgataccgc caagatgttt 60

ggcgcgcagg atctctgtgc toctcttcag tcataggccg gtc gag tgg acc gct 115
 Val Glu Trp Thr Ala
 1 5

ttt ggc acc ctg att ctg ctg aat ttg gtc ggc agt tta tcc ccg ggg 163

Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
 10 15 20
 cct gat acc ttt ttc ctg ctg cgc tta gcc acc cgc tcc aga ggc cac 211
 Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
 25 30 35
 gag atc gat ggc gtc gcc ggc atc gtc acc gga ctg acg gtg tgg gtg 259
 Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
 40 45 50
 acg ctg arg gtc gtg gga gaa ggc ggc ctg ctg acc act tat cag tgg 307
 Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
 55 60 65
 att ctg gga atc atc cag ctg gtc ggc ggc acc tac cta agc ctg att 355
 Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
 70 75 80 85
 ggg tac aag ctg ctg cgc tgg cgc tgg aga gag ctg atc gac gcc cgc 403
 Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
 90 95 100
 cag ttc cgt ctg aac gcc gat gcc cga cct atc cag gat gag gta gaa 451
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
 105 110 115
 gca ctg gga acc cgc act cag gta tat cga caa ggt ctg gcc acc aac 499
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
 120 125 130
 ctg tca acc cgt aac ggt gtc arg tac ctg gag gcc att ctg gat cag 547
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
 135 140 145
 ctg atg caa ggc cac caa caa cgc gtc ctg gag ctg ctg tat ctg atc gtg 595
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
 150 155 160 165
 gag att caa gtg cag acc ttt gtt acc ttc cct gat gtg tgg ctg att 643
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
 170 175 180
 gtc tat aag gag cgt gtc cgc aaa gca atg ctg cgt gca ggt ccc tgg 691
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
 185 190 195
 ttt gac ctg att ggt ggc gtt gtc ttc ctg gtt gtg ggt gtg act ctg 739
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
 200 205 210
 ctg tat gaa ggc ctg acc ggt tta ctg ggc taaaggcata aaaaatgggt 789
 Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
 215 220
 tcc 792

#210: 14
 #211: 223
 #212: FRT

4213- *Corynebacterium glutamicum*

4400- 14

Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
1 5 10 15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
20 25 30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
35 40 45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
85 90 95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
100 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145 150 155 160

Pro Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
180 185 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
195 200 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
210 215 220

4210- 15

4211- 897

4212- DNA

4213- *Corynebacterium glutamicum*

4220-

4221- CDS

4222- (101)..(874)

4223- EMB01796

4400- 15

atgtaactgg atcaggtgga aatgcccgaa aaagtggcgg cgggtggcga gggatggcgg 60

ttggtggcga atcgggtggc tgcactagt cgggtctctt ttg ctc ctt ggc ggt 115
Leu Leu Leu Gly Gly

															1	5	
aac	cct	goc	gag	atc	gac	cag	gtt	tta	ggt	ggc	gat	caa	acc	cag	atc		163
Asn	Pro	Ala	Glu	Ile	Asp	Gln	Val	Leu	Gly	Gly	Asp	Gln	Thr	Gln	Ile		
				10					15					20			
gag	tct	gga	gag	tcc	acc	gga	goc	ggc	gac	ttc	gat	cac	tgc	caa	acc		211
Glu	Ser	Gly	Glu	Ser	Thr	Gly	Ala	Gly	Asp	Phe	Asp	His	Cys	Gln	Thr		
			25					30					35				
gag	gca	gat	goc	aac	goc	agt	gat	gat	tgt	ggc	gtt	tac	tac	acc	tca		259
Gly	Ala	Asp	Ala	Asn	Ala	Ser	Asp	Asp	Cys	Arg	Leu	Tyr	Tyr	Thr	Ser		
			40				45					50					
ttc	tcc	gac	aat	gaa	atg	tgg	cag	act	tgg	gtt	cga	gct	cag	gct	ggc		307
Phe	Ser	Val	Asn	Glu	Met	Trp	Gln	Thr	Leu	Leu	Pro	Ala	Gln	Ala	Gly		
	55					60					65						
atc	gaa	tac	acc	gag	cgc	acc	tgc	act	gtt	tcc	aaa	aac	tac	acc	caa		355
Ile	Gln	Tyr	Thr	Glu	Pro	Thr	Leu	Thr	Leu	Phe	Lys	Asn	Ser	Thr	Gln		
	70				75					80					85		
acc	ggc	tac	ggc	ttc	gat	tct	gag	tcc	act	ggc	cgc	ttt	tac	tgt	cgc		403
Phe	Gly	Cys	Gly	Phe	Ala	Ser	Ala	Ser	Thr	Gly	Pro	Phe	Tyr	Cys	Pro		
				90					95					100			
tca	gac	tac	gat	gat	tat	ttc	gac	tgg	act	tcc	tcc	gat	Gag	arg	cgt		451
Ser	Asp	Gln	Asp	Ala	Tyr	Phe	Asp	Leu	Thr	Phe	Phe	Asp	Gln	Met	Arg		
			105					110					115				
cag	ttc	gct	gca	gaa	aac	goc	acc	ctc	goc	cag	atg	tac	acc	ggc	goc		499
Gln	Phe	Gly	Ala	Glu	Asn	Ala	Pro	Leu	Ala	Gln	Met	Tyr	Ile	Val	Ala		
		120					125					130					
caa	gag	tac	ggc	cac	cac	gtc	caa	aac	ctc	gag	ggc	aca	cgc	gga	ctg		547
His	Gln	Tyr	Gly	His	His	Val	Gln	Asn	Leu	Glu	Gly	Thr	Leu	Gly	Leu		
	135					140					145						
tcc	aat	tac	aac	gat	cgc	ggc	gct	gat	tcc	aac	goc	gtc	arg	atc	gag		595
Ser	Asn	Tyr	Asn	Asp	Pro	Gly	Ala	Asp	Ser	Asn	Ala	Val	Lys	Ile	Glu		
	150				155					160					165		
ttc	cag	goc	gat	tgc	tac	gca	ggc	att	tgc	gct	aat	cac	tac	agg	gaa		643
Leu	Gln	Ala	Asp	Cys	Tyr	Ala	Gly	Ile	Trp	Ala	Asn	His	Ser	Ser	Glu		
			170					175						180			
ggc	cgc	gat	cgc	cta	ctc	caa	cgc	atc	acc	gaa	tct	gag	cgc	gat	tcc		691
Gly	Pro	Asp	Pro	Leu	Leu	Gln	Pro	Ile	Thr	Glu	Ser	Glu	Leu	Asp	Ser		
			185					190					195				
gct	ctc	cgc	gct	gca	acc	goc	gtg	ggc	gac	gac	aat	atc	cag	caa	cga		739
Ala	Leu	Leu	Ala	Ala	Ser	Ala	Val	Gly	Asp	Asp	Asn	Ile	Gln	Gln	Arg		
	200						205					210					
tcc	ggt	goc	gat	gtc	aat	cct	gaa	agg	tgg	act	cac	ggc	tca	tgc	cag		787
Ser	Gly	Gly	Asp	Val	Asn	Pro	Glu	Ser	Trp	Thr	His	Gly	Ser	Ser	Gln		
	215					220					225						
caa	cgc	ana	gac	goc	ttc	ctc	goc	ggc	tac	aac	acc	ggc	cag	atg	agg		835
Gln	Arg	Lys	Asp	Ala	Phe	Leu	Ala	Gly	Tyr	Asn	Thr	Gly	Gln	Met	Ser		
	230				235					240					245		

gac tgc gac ttc ctc ggc ggc ggc gtc tac aac gac gct taaagcattg 884
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
 253 255

atttttgaag tot 897

1210 - 16
 1211 - 153
 1212 - PRT
 1213 - *Corynebacterium glutamicum*

1430 - 16
 Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
 1 5 10 15
 Asp His Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
 21 25 30
 Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
 35 40 45
 Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
 51 55 60
 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80
 Cys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95
 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
 100 105 110
 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125
 Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
 131 135 140
 Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
 145 150 155 160
 Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
 165 170 175
 Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
 180 185 190
 Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
 195 200 205
 Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
 210 215 220
 His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
 225 230 235 240
 Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
 245 250 255

Asp Ala

<010> 17
 <011> 771
 <012> DNA
 <013> Corynebacterium glutamicum

<016>
 <017> FDS
 <022> (101)1.743)
 <026> EX001207

<010> 17
 tttctgatac tcaacggcag agcgggtttt gttacagcgc gtaaacgtgtg accttgaaaa 60

cttttgatac aattcgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
 Val Ser Arg Ile Tyr
 1 5

tat tgt tcc caa caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
 Asp Gln Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
 10 15 20

tat tca tcc aaa gac ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
 25 30 35

tat tga tcc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
 40 45 50

tat tcc tcc aaa caa cgt ggc ccc gat atg ccc gtc cca gtg ccc gtc 307
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
 55 60 65

pro tgc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
 Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
 70 75 80 85

tca aac tcc ctt gtg gag ggc ttc tgg ctt ggt gga ctg tcc atc atc 403
 Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
 90 95 100

gtc tcc cag gca cca agc ctt ccc tgg aac ctt ggc gat acc cgt ggc 451
 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
 105 110 115

acc cta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
 120 125 130

guc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
 135 140 145

act cct tca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
 150 155 160 165

gtc ggt gtc tac ctc gat ggt ggc gaa tgc ggc ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180

acc atc gtg gat att tca ggc acc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195

gcc atc agc gca gaa cgc gtc ggc gaa gta ctt gga gtg tgg gca gaa 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
 200 205 210

agc ctg agc taaatggag tgggttggc ggg 771
 Ser Leu Arg
 215

<210> 18
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 18
 Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
 1 5 10 15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
 20 25 30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Gln Ala Arg Gln
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu

195

200

205

Gly Val Ser Ala Glu Ser Leu Arg
110 215

0010- 19
0011- 1026
0012- DNA
0013- Corynebacterium glutamicum

0010-
0011- CDS
0012- (111)..(1003)
0013- RXC00657

04 0- 19

ttgggtagtg ggtatccggg cttaacttag aggtgttaga gatcatgagt ttccacgaac 60

tttaacggcag gattcaacaa tcatatgaag gtccacccgac atg agc act gaa gac 115
Met Ser Thr Glu Asp
1 5

att ctg gtc gta gca gta tat ggc tgg gac gcc tca aaa caa gct gtt 163
Leu Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
10 15 20

acc agc gct gca aat acc tcc aac aaa cgt ggc att cca ctt cgc ttg 211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
25 30 35

gtt tcc agc taa acc atg cct cag ttc ctg taa tca gac gag gga atg gtt 269
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
40 45 50

tca cca caa gag ctt ttc tat gac ctg cag gcc gaa gcc ctg gaa aag 307
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
55 60 65

att caa gaa gcc cgt gac atc gcc cat gag gta gcc cca gaa atc aag 365
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
70 75 80 85

atc ggg cac acc atc gct caa ggc agt ccc atc gac atg ctg ttg gaa 403
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
90 95 100

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctg gcc 461
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
105 110 115

gga atc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc 499
Gly Leu Ser Gly Met Val Met Ser Val Ser Gly Ala Val Val Ser
120 125 130

cac cca aag tgt cca gtc att gtt gtc cgt gaa gac agc gca gtc aac 547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
135 140 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu

35										90					95				
Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly																			
			100					105							110				
Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser																			
			115					120							125				
Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu																			
			130					135							140				
Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly																			
			145					150							155		160		
Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala																			
			165												170		175		
Gln Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met																			
			180												185		190		
Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln																			
			195												200				
Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg																			
			205												210				
Ser Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile																			
			215												220				
Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn																			
			225												230		235		
Ala Glu Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly																			
			240												245		250		
Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys																			
			255												260		265		
Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys																			
			270												275		280		

01100: 21

01110: 1159

01120: DNA

01130: Corynebacterium glutamicum

02100:

02110: CDS

02120: (101)..(1036)

02130: EX000552

04000: 21

gggcaaaacaa ggcagcaaaag ctgatccaa ttgaagcctt gggttatgag taaaagcctc 60

gtttttaagg tagccacaca tggcaactaga ctgaagaact ctg gct acc tca aaa 115
Val Ala Thr Ser Lys
1 5

att ctt ctt tat tac gca ttc acc ccg ctc tet gac cct aaa gcg gtt 163
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val

10						15						20						
cag	ctg	tgg	cag	cgt	gag	ctc	tgc	gag	tca	ctg	aat	ctt	cgt	ggc	cgc	211		
Gln	Leu	Trp	Gln	Arg	Glu	Leu	Cys	Glu	Ser	Leu	Asn	Leu	Arg	Gly	Arg			
			25				30				35							
atc	ctg	atc	tcc	act	cac	gac	atc	aat	gga	acc	gtg	ggc	gga	gat	att	259		
Ile	Leu	Ile	Ser	Thr	His	Gly	Ile	Asn	Gly	Thr	Val	Gly	Gly	Asp	Ile			
			40				45				50							
gat	gat	tgc	aag	ggg	tac	att	aaa	tac	acc	cgc	gag	tac	cct	ggc	ttc	307		
Asp	Asp	Cys	Lys	Ala	Tyr	Ile	Lys	Lys	Thr	Arg	Glu	Tyr	Pro	Gly	Phe			
			55				60				65							
aac	cgc	atg	cac	ttt	agg	tac	tcc	tac	ggt	ggc	gct	gag	gat	ttt	cct	335		
Asn	Arg	Met	Gln	Phe	Lys	Trp	Ser	Glu	Gly	Gly	Ala	Glu	Asp	Phe	Pro			
			70				75				80				85			
aag	ctg	agt	gtc	aaa	gac	cct	gat	tac	atc	gtt	gac	ttc	ggc	gct	cct	403		
Lys	Leu	Ser	Val	Lys	Val	Arg	Asp	Glu	Ile	Val	Ala	Phe	Gly	Ala	Pro			
			90				95				100							
gat	gag	ctc	aaa	gtg	att	gaa	aac	ggc	ctc	gtc	ggt	ggc	ggc	gtt	cac	451		
Asp	Glu	Leu	Lys	Val	Asp	Gln	Asn	Gly	Val	Val	Gly	Gly	Gly	Val	His			
			105				110				115							
ctg	aaa	cct	cag	cag	tcc	aat	gag	ttt	tgc	gaa	ggc	cgt	ggc	gat	gaa	499		
Leu	Lys	Pro	Gln	Gln	Val	Asn	Glu	Leu	Val	Glu	Ala	Arg	Gly	Asp	Glu			
			120				125				130							
gtt	gtg	tcc	tcc	gac	cct	cct	aac	cct	atg	gaa	ggc	cag	att	ggc	aag	547		
Val	Val	Phe	Phe	Asp	Gly	Arg	Asn	Ala	Met	Glu	Ala	Gln	Ile	Gly	Lys			
			135				140				145							
ttc	aag	gac	gct	gtt	tcc	cct	gac	tta	aaa	acc	act	cac	gat	ttc	atc	595		
Phe	Lys	Asp	Ala	Val	Val	Pro	Asp	Val	Glu	Thr	Thr	His	Asp	Phe	Ile			
			150				155				160				165			
gaa	gaa	att	gag	tct	aaa	aaa	tac	tac	gat	ctc	aaa	gac	aac	cct	gtg	643		
Ala	Glu	Ile	Gln	Ser	Gly	Lys	Tyr	Asp	Asp	Leu	Lys	Asp	Lys	Pro	Val			
			170				175				180							
gtc	acc	tac	tgc	acc	ggc	gga	att	cgt	tgt	gag	atc	ctg	agt	tca	ctc	691		
Val	Thr	Tyr	Cys	Thr	Gly	Gly	Ile	Arg	Cys	Glu	Ile	Leu	Ser	Ser	Leu			
			185				190				195							
atg	atc	aac	cgt	ggc	ttc	aaa	gag	gtc	tac	caa	atc	gat	ggc	ggc	atc	739		
Met	Ile	Asn	Arg	Gly	Phe	Lys	Glu	Val	Tyr	Gln	Ile	Asp	Gly	Gly	Ile			
			200				205				210							
gtt	cgc	tac	ggc	gag	cag	ttt	ggc	aac	aag	ggc	ctg	tgg	gaa	ggc	tcc	787		
Val	Arg	Tyr	Gly	Glu	Gln	Phe	Gly	Asn	Lys	Gly	Leu	Trp	Glu	Gly	Ser			
			215				220				225							
ctc	tac	gtt	ttc	gat	aag	cgc	atg	cac	atg	gaa	ttc	ggc	gag	gat	tac	835		
Leu	Tyr	Val	Phe	Asp	Lys	Arg	Met	His	Met	Glu	Phe	Gly	Glu	Asp	Tyr			
			230				235				240				245			
aaa	gag	gtc	ggc	cac	tac	atc	cac	tgc	gat	act	cct	acc	aac	aaa	ttt	883		
Lys	Glu	Val	Gly	His	Cys	Ile	His	Cys	Asp	Thr	Pro	Thr	Asn	Ly.	Phe			
			250				255				260							

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
 265 270 275
 cct gat tgc ttc gcc aat gtt gag acc cgt cat tga aag cgc gaa cgc 979
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
 280 285 290
 tgt gca gca att gct gcg gat ttc gct gag caa gga att gat cgc ctc 1027
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
 295 300 305
 gtc act tct taaaaagggt atgggtgctg ggt 1059
 Val Thr Ser
 310

<210> 12

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

Val Ala Phe Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
 1 5 10 15
 Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
 2 5 10
 Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
 30 40 45
 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
 50 55 60
 Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65 70 75 80
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
 100 105 110
 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
 130 135 140
 Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
 145 150 155 160
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
 165 170 175
 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
 180 185 190
 Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln

195	200	205
Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly		
210	215	220
Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu		
225	230	235
Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr		
245	250	255
Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu		
260	265	270
Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His		
275	280	285
Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln		
290	295	300
Gly Ile Asp Pro Leu Val Thr Ser		
305	310	

<210>=13
 <211>=1336
 <212>=CNA
 <213>=Corynebacterium diphtheriae

<220>
 <221>=CDS
 <222>=1010111(1363)
 <223>=EXA10554

<410>=13
 ctgttcagaa agaaaacact cctctggata gctagacaca gttttaaaag gttagattga 60
 ggaggtaact gttagaacgt agatcgaaag gtgcacaaag gtc gcc ctg gtc gta 115
 Val Ala Leu Val Val
 1 5
 cag aaa tat ggc ggt tcc tgg ctt gag agt ggc gaa gcc att aga aac 163
 Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn
 10 15 20
 gtc tct gaa cgc atc gtt gcc acc aag aag gct gga tat gat gtc gtc 211
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val
 25 30 35
 gtt gtc tgc tcc gca atg gga gac acc aag gat gaa ctt cta gaa ctt 259
 Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
 40 45 50
 gca ggc gca gtc aat ccc gtt cgc cca gct cgt gaa atg gat atg ctc 307
 Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu
 55 60 65
 ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 70 75 80 85

gag	too	ctt	ggc	gca	gaa	gac	caa	tet	ttc	acg	ggc	tct	cag	gct	ggt	403
Glu	Ser	Leu	Gly	Ala	Glu	Ala	Gln	Ser	Phe	Thr	Gly	Ser	Gln	Ala	Gly	
			90						95						100	
gtg	ctc	acc	acc	gag	ggc	gac	gga	aac	gca	ggc	att	gtt	gat	gac	act	461
Val	Leu	Thr	Thr	Glu	Arg	His	Gly	Asn	Ala	Arg	Ile	Val	Asp	Val	Thr	
			105					110						115		
cca	ggt	ggt	gtg	ggt	gaa	gca	ctc	gat	gag	ggc	aag	atc	tgc	att	ggt	469
Pro	Gly	Arg	Val	Arg	Glu	Ala	Leu	Asp	Glu	Gly	Lys	Ile	Cys	Ile	Val	
			120					125					130			
gct	ggt	ttc	cag	ggt	ggt	aat	aaa	gaa	acc	ggc	gat	gtc	acc	acg	ttg	547
Ala	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg	Asp	Val	Thr	Thr	Leu	
			135					140					145			
ggt	ggt	ggt	ggt	ggt	tct	gac	acc	acc	gca	ggt	ggg	ttg	gca	gat	ggt	548
Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala	Leu	Ala	Ala	Ala	Leu	
			150					155				160			165	
aac	gct	gat	gtg	ggt	gag	att	tac	tgc	gac	ggt	gac	ggt	gtg	tat	acc	643
Asn	Ala	Asp	Val	Cys	Glu	Ile	Pyr	Ser	Asp	Val	Asp	Gly	Val	Tyr	Thr	
			170						175					180		
gct	gac	ggg	ggc	atc	ggt	ggt	aac	gca	gag	aag	ggg	gaa	aag	ctc	agc	661
Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys	Leu	Glu	Lys	Leu	Ser	
			185					190						195		
ttc	gaa	gaa	atg	atg	gaa	ggt	ggt	ggt	ggg	ttc	gag	att	ttg	gtg		769
Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val	
			205					205					210			
ctc	ggc	ggt	ggt	gaa	tac	ggt	ggt	gca	ttc	aac	gta	cca	gtt	ggc	gta	787
Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val	
			215					220								
ggc	tgc	tct	tat	agt	aac	gat	ggc	ggc	act	ttg	att	ggc	ggc	tct	atg	888
Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu	Ile	Ala	Gly	Ser	Met	
			235					240						245		
gag	gat	att	ggt	gtg	gaa	gaa	gca	gtc	gtt	acc	ggt	gtc	gca	acc	gac	883
Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr	Gly	Val	Ala	Thr	Asp	
			250					255						260		
aag	too	gaa	ggc	aaa	gta	acc	ggt	ctg	ggt	att	ttc	gat	aag	cca	ggc	961
Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Leu	Gly	Ile	Ser	Asp	Lys	Pro	Gly	
			265					270						275		
gag	gct	ggg	aag	ggt	ttc	ggt	ggg	ttg	gct	gat	gca	gaa	atc	aac	att	979
Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile	
			280					285					290			
gac	atg	ggt	ctg	cag	aac	gtc	tct	tct	gta	gaa	gac	ggc	acc	acc	gac	1027
Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu	Asp	Gly	Thr	Thr	Asp	
			295					300					305			
atc	acc	ttc	acc	tgc	ggt	ggc	ggc	ggc	ggc	ggc	atg	gag	atc			1075
Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ser	Asp	Gly	Arg	Arg	Ala	Met	Glu	Ile	
			310					315					320		325	
ttg	aag	aag	ctt	cag	ggt	cag	ggc	aac	tgg	acc	aat	gtg	ctt	tac	gac	1123

Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp
 330 335 340
 gag gag gtc ggc aaa atc tcc ttc gtg ggt gct ggc atg aag tct cac 1171
 Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
 345 350 355
 cca agt att acc gca gag ttc atg gaa gct atg ggc gat gtc aac gtg 1219
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
 360 365 370
 aac atc gaa ttg att tcc acc tct gag att agt att tcc gtg atg atc 1267
 Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
 375 380 385
 cgt aac gct gat atg gat gct gct gca cgt gca ttg cat gag cag ttc 1315
 Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
 390 395 400 405
 cag atg tcc ggc gaa aac gaa ggc gtc gtt cat gca ggc acc gga cgc 1363
 Gln Leu Gly Gly Glu Asp Glu Ala Val Tyr Ala Gly Thr Gly Arg
 410 415 420
 taaattttta aaggagtagt ttt 1386

<110> 24
 <111> 421
 <112> PR2
 <113> Corynebacterium glutamicum

<110> 24
 Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
 1 5 10 15
 Gln Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Pro Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Asp Ala Met Glu Ile Leu Lys Lys Leu Glu Val Gln Gly Asn Trp Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415
 Ala Gly Thr Gly Arg
 420

01108: 15
 01110: 1155
 01120: DNA
 01130: Corynebacterium glutamicum

02200:
 02210: CDS
 02220: (101)..(1132)

4273 PXA:0553

400: 25

ttcacgtgc attgcatgag cagttccagc tgggscggcga agacgaagcc gtcgtttatg 60

taggcacacgg agcgtaaaagt tttaaaggag tagtattaca atg acc acc atc gca 115
 Met Thr Thr Ile Ala
 1 5

ggt gtt ggt gga acc ggc cag gtc ggc cag gtt atg ggc acc gtt ttg 163
Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu
10 15 20

gaa gag agc aat ttc cca gct gac act gtt cgt ttc ttc gct ccc cca 211
Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro
25 30 35

cgt tcc gga ggc cgt aag att gaa ttg cgt ggc acg gaa atc gag gta 259
Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val

 40 46 52

1aa daa att acg gag gaa acc gag gag tcc ctg aag gaa atc gaa gtt 307
 Gln Asp Ile Thr Gln Ala Thr Gln Gln Ser Leu Lys Asp Ile Asp Val
 35 60 65

183 186 189 192 195 198 201 204 207 210 213 216 219 222 225 228 231 234 237 240 243 246 249 252 255 258 261 264 267 270 273 276 279 282 285 288 291 294 297 300 303 306 309 312 315 318 321 324 327 330 333 336 339 342 345 348 351 354 357 360 363 366 369 372 375 378 381 384 387 390 393 396 399 402 405 408 411 414 417 420 423 426 429 432 435 438 441 444 447 450 453 456 459 462 465 468 471 474 477 480 483 486 489 492 495 498 501 504 507 510 513 516 519 522 525 528 531 534 537 540 543 546 549 552 555 558 561 564 567 570 573 576 579 582 585 588 591 594 597 600 603 606 609 612 615 618 621 624 627 630 633 636 639 642 645 648 651 654 657 660 663 666 669 672 675 678 681 684 687 690 693 696 699 702 705 708 711 714 717 720 723 726 729 732 735 738 741 744 747 750 753 756 759 762 765 768 771 774 777 780 783 786 789 792 795 798 801 804 807 810 813 816 819 822 825 828 831 834 837 840 843 846 849 852 855 858 861 864 867 870 873 876 879 882 885 888 891 894 897 900 903 906 909 912 915 918 921 924 927 930 933 936 939 942 945 948 951 954 957 960 963 966 969 972 975 978 981 984 987 990 993 996 999 1002 1005 1008 1011 1014 1017 1020 1023 1026 1029 1032 1035 1038 1041 1044 1047 1050 1053 1056 1059 1062 1065 1068 1071 1074 1077 1080 1083 1086 1089 1092 1095 1098 1101 1104 1107 1110 1113 1116 1119 1122 1125 1128 1131 1134 1137 1140 1143 1146 1149 1152 1155 1158 1161 1164 1167 1170 1173 1176 1179 1182 1185 1188 1191 1194 1197 1200 1203 1206 1209 1212 1215 1218 1221 1224 1227 1230 1233 1236 1239 1242 1245 1248 1251 1254 1257 1260 1263 1266 1269 1272 1275 1278 1281 1284 1287 1290 1293 1296 1299 1302 1305 1308 1311 1314 1317 1320 1323 1326 1329 1332 1335 1338 1341 1344 1347 1350 1353 1356 1359 1362 1365 1368 1371 1374 1377 1380 1383 1386 1389 1392 1395 1398 1401 1404 1407 1410 1413 1416 1419 1422 1425 1428 1431 1434 1437 1440 1443 1446 1449 1452 1455 1458 1461 1464 1467 1470 1473 1476 1479 1482 1485 1488 1491 1494 1497 1500 1503 1506 1509 1512 1515 1518 1521 1524 1527 1530 1533 1536 1539 1542 1545 1548 1551 1554 1557 1560 1563 1566 1569 1572 1575 1578 1581 1584 1587 1590 1593 1596 1599 1602 1605 1608 1611 1614 1617 1620 1623 1626 1629 1632 1635 1638 1641 1644 1647 1650 1653 1656 1659 1662 1665 1668 1671 1674 1677 1680 1683 1686 1689 1692 1695 1698 1701 1704 1707 1710 1713 1716 1719 1722 1725 1728 1731 1734 1737 1740 1743 1746 1749 1752 1755 1758 1761 1764 1767 1770 1773 1776 1779 1782 1785 1788 1791 1794 1797 1800 1803 1806 1809 1812 1815 1818 1821 1824 1827 1830 1833 1836 1839 1842 1845 1848 1851 1854 1857 1860 1863 1866 1869 1872 1875 1878 1881 1884 1887 1890 1893 1896 1899 1902 1905 1908 1911 1914 1917 1920 1923 1926 1929 1932 1935 1938 1941 1944 1947 1950 1953 1956 1959 1962 1965 1968 1971 1974 1977 1980 1983 1986 1989 1992 1995 1998 2001 2004 2007 2010 2013 2016 2019 2022 2025 2028 2031 2034 2037 2040 2043 2046 2049 2052 2055 2058 2061 2064 2067 2070 2073 2076 2079 2082 2085 2088 2091 2094 2097 2100 2103 2106 2109 2112 2115 2118 2121 2124 2127 2130 2133 2136 2139 2142 2145 2148 2151 2154 2157 2160 2163 2166 2169 2172 2175 2178 2181 2184 2187 2190 2193 2196 2199 2202 2205 2208 2211 2214 2217 2220 2223 2226 2229 2232 2235 2238 2241 2244 2247 2250 2253 2256 2259 2262 2265 2268 2271 2274 2277 2280 2283 2286 2289 2292 2295 2298 2301 2304 2307 2310 2313 2316 2319 2322 2325 2328 2331 2334 2337 2340 2343 2346 2349 2352 2355 2358 2361 2364 2367 2370 2373 2376 2379 2382 2385 2388 2391 2394 2397 2400 2403 2406 2409 2412 2415 2418 2421 2424 2427 2430 2433 2436 2439 2442 2445 2448 2451 2454 2457 2460 2463 2466 2469 2472 2475 2478 2481 2484 2487 2490 2493 2496 2499 2502 2505 2508 2511 2514 2517 2520 2523 2526 2529 2532 2535 2538 2541 2544 2547 2550 2553 2556 2559 2562 2565 2568 2571 2574 2577 2580 2583 2586 2589 2592 2595 2598 2601 2604 2607 2610 2613 2616 2619 2622 2625 2628 2631 2634 2637 2640 2643 2646 2649 2652 2655 2658 2661 2664 2667 2670 2673 2676 2679 2682 2685 2688 2691 2694 2697 2700 2703 2706 2709 2712 2715 2718 2721 2724 2727 2730 2733 2736 2739 2742 2745 2748 2751 2754 2757 2760 2763 2766 2769 2772 2775 2778 2781 2784 2787 2790 2793 2796 2799

Phe Met Lys Phe Gln Gln Asn Ile Val Glu Asp Asn Ser Ser Ala Trp Arg 406
Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg
 90 95 100

449 gag gac gac gag gtt cca cta atc gtc tct gag gtc aac cct tcc gac 451
 Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp
 105 110 115

tag gat tdc cag gtc aag ggc att att gag aac cct aar tgc acc acc 499
 Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr
 120 125 130

Met Arg Arg Arg Ser Gly Arg Asp Ser Thr Ser Gln Gln Gln Gly Thr 547
Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu
135 140 145

gta aag att cac gtt tcc tct cac gag gct gtt tcc ggt tct ggt ctt 595
Val Iys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu
150 155 160 165

gca ggt gtg gaa acc ttg gca aag cag gtt got gca gtt gga gac cac 645
Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His
170 175 180

aaq gtt gag ttg gtc cat gat gga gag got got gac gaa ggc gat gtc 691
 Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val
 135 190 195

Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly 739
200 205 210

aac ctc gtc gat gac ggc acc ttc gaa acc gat gaa gag cag aag ctg 787
 Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp Glu Glu Gln Lys Leu
 215 220 225
 cgc aac gaa ttc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835
 Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser
 230 235 240 245
 ggc acc ttc gtc cgc gtc cgc gtt ctc acc ggc ccc acc ctg acc att 883
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
 250 255 260
 ccc gcc gaa ttc gat aag gca atc acc gtc gac cag ggc cag gag atc 931
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
 265 270 275
 ttg ggt gcc gat tca gcc gtc aag ctt gtc gac gtc cca acc cca ctt 979
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
 280 285 290
 gca gct gcc gcc att gac gaa ttc ctc gtt gcc cgc atc cgt cag gac 1027
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
 295 300 305
 ttc act gtc gac gat aac cgc ggt ctc gtt ctc gtc gta tct gcc gac 1075
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
 310 315 320 325
 acc ttc cgc aag ggt cct gcc cta aac acc atc cag atc gct gag ctg 1123
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Phe Ile Gln Ile Ala Glu Leu
 330 335 340
 ctg att aag tcaaaaccgc caattaaaaa ctc 1155
 Leu Val Lys

0310 26
 0311 344
 0312 PRT
 0313 Corynebacterium glutamicum

0400 26
 Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val
 1 5 10 15
 Met Arg Thr Leu Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
 20 25 30
 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
 35 40 45
 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
 50 55 60
 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
 65 70 75 80
 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
 85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
 100 105 110
 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
 115 120 125
 Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
 130 135 140
 Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
 145 150 155 160
 Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
 165 170 175
 Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
 180 185 190
 Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
 195 200 205
 Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
 210 215 220
 Glu Gln Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
 225 230 235 240
 Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
 245 250 255
 His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp
 260 265 270
 Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp
 275 280 285
 Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
 290 295 300
 Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
 305 310 315 320
 Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
 325 330 335
 Gln Ile Ala Glu Leu Leu Val Lys
 340

<210> 27

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (59)..(608)

<223> EXA02843

<400> 27

ccattgcgc ggaggtggca ccccttcgga ctggaactga taggcgata gaaattatc 60

tgggagtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
 1 5 10
 acc agc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 153
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
 15 20 25 30
 cag tcc ggc ctg aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
 35 40 45
 acc agc aaa atc gtg acg aca act atc gac acc gac gca gcc acc acc 251
 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
 50 55 60
 gac acc tac gat gca tgg ctg ggc ctt caa ctc ctc tcc caa ggc gtt 302
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
 65 70 75
 ttc agc cct caa acc atc aac cta gac ggc att ttc ggc ctg ctc aac 351
 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
 80 85 90
 cat ctg gtg tgg acc aac ttc gga cgg tgc gca gtt gac ggt ttc gca 391
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
 95 100 105 110
 ttc acc agc ggc ggc ctg tca ggc cga ggc caa gtt acc gtt tat agc 446
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
 115 120 125
 ttc aac aac ttc cca cgc atg gtc gac tat gtg gtt ccc acc ggc gtg 494
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
 130 135 140
 agc atc gct gac gcc gac cgc gtc cga ctt ggc ggc tac ctg gca gat 542
 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
 145 150 155
 ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
 160 165 170
 ttc agc gct tcc atg gtt 605
 Leu Gly Ala Ser Met Val
 175 180

0110 28

0111 180

0112 PRT

0113 - Corynebacterium glutamicum

0400 28

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
 1 5 10 15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
 20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
 35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175

Ala Ser Met Val
 180

0000 29
 0010 1231
 0020 DNA
 0030 Corynebacterium glutamicum

0000
 0010 CDS
 0020 (101)..(1207)
 0030 EXA12022

0400 29
 taatgggat tccaactgct tgggttcgc gaatgtttc actcatttt taatcgaccg 60

cttcaatcat gtattaaacta aggtttgtag gcttaaaact gtg aac tct gaa ctc 115
 Val Asn Ser Glu Leu
 1 5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
 10 15 20

tgg gta gat ata cgg agt cgg tca ggt cag gaa aag cag att gct gat 211
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
 25 30 35

gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
 40 45 50

ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc	307
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala	
35 60 65	
tgc agg gtc atg ctt gct ggt cat atc gat aca gtc ccg atc gag gac	335
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtc gaa gac ggc atc atg tat ggc tgt ggc aac	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gag gtc tat ttg cat act ttt gcc aac	431
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acc tgc act gag att aaa cat gat ctg acg ctg att gag tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gag tgc gag gaa gtt gct gat aac ctc aat ggt ttg ggc cac att cgc	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat cgc gag tgg ttg gag gct gat ttg gag ttg ttg ggt gag	585
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
act act ggc ggc tgg att aac ggc ggc tgg cag ggc aat ctg ggc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Glu Gly Asn Leu Arg Ile	
170 175 180	
aaa gtc acg gag cat ggt gtc cgt gcc cat tgc gag aca agc tgg ttg	681
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat gag atg cat aag ttg tgc cgc atc att tgc aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
ggc tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tgc ggc gtc gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gag ctg gag tgg atg aac ctc aac ttc cgt ttc ggc ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag ggc atc gag cat gtc gtc gaa acg ctt gag ctt gag	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gag ggc atc gaa tgg gcc gta gaa gac ggc gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtc aca agc ggc ctt atc gac gcc gtc	1027

Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val
 295 300 305
 ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt 1075
 Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
 310 315 320 325
 att ttc ggc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca 1123
 Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
 330 335 340
 att ttc ggc cat aaa cgc gac gag cag tgc cca gtg gag caa atc acc 1171
 Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Gln Gln Ile Thr
 345 350 355
 cat gtg gca gca att atg aag cag tac ctg agc gag taaccgcatt 1217
 Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
 360 365
 cgggttacc gtg 1230

 110> 40
 111> 69
 112> PR7
 113> Corynebacterium glutamicum

 1208 40
 Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile
 1 5 10 15
 Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
 20 25 30
 Lys Glu Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
 35 40 45
 Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
 5 55 60
 Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
 65 70 75 80
 Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
 85 90 95
 Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
 100 105 110
 His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
 115 120 125
 Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
 130 135 140
 Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
 145 150 155 160
 Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
 180 185 190
 Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile
 195 200 205
 Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly
 210 215 220
 Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val
 225 230 235 240
 Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg
 245 250 255
 Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu
 260 265 270
 Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp
 275 280 285
 Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly
 290 295 300
 Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp
 305 310 315 320
 Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe
 325 330 335
 Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro
 340 345 350
 Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser
 355 360 365

Gln

<110> 31
 <111> 1054
 <112> DNA
 <113> Corynebacterium glutamicum

<114>
 <115> CDS
 <116> (111)..(1036)
 <117> EXA00044

<400> 31
 attacctcag ccttccaagc tcatgatgca ttacttaaaa actgcagaca cttgaaaaac 60

ttctcaccac cactcgttcc ctcaaccac aaggagcaac atg gct tcc gca act 115
 Met Ala Ser Ala Thr
 1 5

ttc acc ggc gtg atc ccg ccc gta atg acc cca ctc cac gcc gac ggc 163
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
 10 15 20

agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat	211
Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn	
25 30 35	
ggg ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gca gca	259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala	
40 45 50	
ttc ctc aac cgc ggc cag cgc aaa ctc gca ctg aac aac atc atc gag	307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu	
55 60 65	
cac aac gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc	355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr	
70 75 80 85	
act gct ggc gtc att gag ctc gtc gaa gat ggc ctg gag gct ggt ggc	403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala	
9 95 100	
gaa ggc ctc gtt gct act gca act ttc tac aac cgc aac cac gat gtc	451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val	
105 110 115	
gaa att gaa gaa cac ttc cgc aag atc cac ggc ggc gct cca gat att	499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu	
120 125 130	
cca ctg att gcc tac aac att cca gtc tcc gtc cac tcc aac ctc aac	547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn	
135 140 145	
cca gtc atg att ttc aag ctc ggc aag gat ggc gtt ctt gca ggc aac	595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr	
150 155 160 165	
aag gat tcc agt ggc aat gat gtc gca atc cgc tca ctg atc gat gct	643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala	
170 175 180	
cgt gat gat gct gga ctc act gag cag ttc aag atc ctc aac ggc agc	691
Arg Asp Asp Ala Gly Leu Thr Gln Gln Phe Lys Ile Leu Thr Gly Ser	
185 190 195	
gaa aac aac gtt gat ttc gcc tac ctt ggc ggt gcc gat gga gtt gtc	739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val	
200 205 210	
cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa	787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys	
215 220 225	
ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc	835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg	
230 235 240 245	
atc aac cac ctc ttc cac atc gtc ttc gtc gga gac aac tcc cat atg	883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met	
250 255 260	
tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac	931

Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
265 270 275

ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
280 285 290

agc gac gaa gaa act gct ggc att cac gcc att gtt gat gaa ttc ctg 1027
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
295 300 305

tac acc gct taaggccac acctcatgac tga 1059
Tyr Thr Ala
310

<L10> 12

<L11> 112

<L12> BRT

<L13> Corynebacterium glutamicum

<400> 12

Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro
1 5 10 15

Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
20 25 30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Glu Arg Lys Leu Ala Leu
50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala
225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly
245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys
260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val
275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile
290 295 300

Val Asp Glu Phe Leu Tyr Thr Ala
305 310

(210) 33

(211) 167

(212) CNA

(213) *Torynebacterium glutamicum*

(220)

(221) CDS

(222) (101) 844)

(223) EXA00863

(400) 33

aacgatcagt taggtatgga taccagcacc ttctgaaagg gtacgtctag actggtgggc 60

gtttcaaaa ctcttgccc caccgaaatg aaggagcata atg gga atc aag gtt 115
Met Gly Ile Lys Val
1 5

ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala
10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc gcc gtc gac 211
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp
25 30 35

gat gat ttg agc ctt ctg gta gac aac gcc gct gaa gtt gtc gtt gac 259
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp
40 45 50

ttc aac act cct aac gct gtg atg gcc aac ctg gag ttc tgc atc aac 307
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn
55 60 65

aac gcc att tct ggc gtt gtt gga acc acg gcc ttc gat gat gct cgt 355
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg
70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
 65 70 75 80
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
 85 90 95
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
 100 105 110
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
 115 120 125
 Gln Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
 130 135 140
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
 145 150 155 160
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
 165 170 175
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
 180 185 190
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
 195 200 205
 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
 210 215 220
 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
 225 230 235 240
 Gly Leu Glu His Tyr Leu Gly Leu
 245

010: 35
 011: 373
 012: DNA
 013: *Corynebacterium glutamicum*

015:
 016: CDS
 017: (101)..(350)
 018: EXA00364

000: 35
 acagacacca ggctagctcg taggaactga gcattacctt ggctgtgaaa ggctcatttc 60
 acagaggggt ggaatttttt aaaaggagag tttaaaggct gtg gcc gaa caa gtt 115
 Val Ala Glu Gln Val
 1 5
 aaa ttg agc gtg gag ttg ata ggc tgc agt tct ttt act cca ccc gct 163
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
 10 15 20
 gat gtt gag tgg tca act gat gtt gag ggc ggc gaa gca ctg gtc gag 211
 Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
 25 30 35

ttt ggg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259
 Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
 40 45 50

act gct tcc aat gct ggg tat ctg cgc cac atc atg gaa gtg ggg cac 307
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
 55 60 65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 315
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
 70 75 80 85

tct cgg tcc gag acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
 90 95 100

tct caa ttg tct cag cgt ttc gtg cac agc gga gaa ttg gaa gta gtg 451
 Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
 105 110 115

gtg ccc tct ctg atc gat gaa gat ccg cag ttg ctt gaa ctt ttc atg 499
 Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
 120 125 130

aac gcc atg gat gag tct cag ttc gct ttc aat gag ctg ctt aat ggg 547
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
 135 140 145

ttg gaa gaa aaa ctt ggc gat gaa ccg aat gaa ctt tta agg aaa aag 595
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
 150 155 160 165

aca gct cgt caa gca gct cgc gct gtg ctg ttc aac gct aca gag tcc 643
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
 170 175 180

aga atc ttg gtg tct gga aac ttc cgc acc tgg aag cat ttc att ggc 691
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
 185 190 195

ttg cga gcc apt gaa cat gaa gac gtc gaa atc cgc gaa gta ggc gta 739
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
 200 205 210

gaa tgt tta aga aag ctg cag gta gca ggc cca act gtt ttc ggt gat 787
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
 215 220 225

ttt gag att gaa act ttg gca gac gga ttg caa atg gca aca agc ccg 835
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
 230 235 240 245

tat gtc atg gac ttt taacgcaaaag ctcacaccca cga 873
 Tyr Val Met Asp Phe
 250

<210> 16
 <211> 250
 <212> PRT

<213> Corynebacterium glutamicum

<100> 36

Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Ile Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Arg Ala Val Leu Pro
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

<10> 37

<11> 408

<12> DNA

<13> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> EXA02843

4400 - 37

ccccattgcg ggagggtcgca ccccttcgga cttgaactga taggcggata gaaattattc 60

tggaagtc atg aat aat gct tcc gca acc gga att gca aca ctg acc tcc 110
 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
 1 5 10

acc ggc gac gtc ctg gac gtc tgg tat cca gaa atc ggg tcc acc gac 150
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
 15 20 25 30

cag tcc gag ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 200
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
 35 40 45

ccc cgc aaa atc gtc aag aca aat atc gac acc gac gca gcc ctc acc 250
 Phe Arg Lys Ile Val Phe Thr Thr Ile Asp Thr Asp Ala Ala Pro Phe
 50 55 60

ccc acc ttc gat gca tgg ctg cgc ctt cca cta cta tcc cca cgc gtc 300
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
 65 70 75

ccc ggc cct cca acc aac aac cta gac ggc att ttc ggc cta cta aac 350
 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
 80 85 90

atc ttc gtc tgg acc aac ttc gga cgc tgc gca gtt gac ggt ttc gca 400
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
 95 100 105 110

atc acc cgc gag cgc ctg cca cgc cga ggc caa gtt acc gtt tat agc 450
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
 115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtc gtt ccc tcc ggc gtc 500
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
 130 135 140

gpc atc ggt gac gcc gac cgc gtc cga ctt ggc ggc tac ctg gca gat 550
 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
 145 150 155

gtc acc acc gtc atg cca gag ggc ttc gtc aac ttc aac gct ggc acc 600
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
 160 165 170

ctc gcc gct tcc atg gtt 608
 Leu Gly Ala Ser Met Val
 175 180

4210 - 38

4211 - 120

4212 - PRT

4213 - *Corynebacterium glutamicum*

4400 - 38

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
 1 5 10 15

[illegible]

0010 - 39
0011 - 1143
0012 - DNA
0013 - *Corynebacterium glutamicum*

```

CCL0 -
CCL1 - CDS
CCL2 - (101)..(1120)
CCL3 - EXNO1350

```

```

04000-39
aataagatcag cgcattcgtg gtggaaccaa aagggtcaac aatacgaac gtccgcttcc 60
ggtctgatg aaagagatgt cccatgaatc tcatctaagt atg cat ctg ggt aag 115
Met His Leu Gly Lys
1 5
ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
10 15 20
acc aac atc cgc gta gct atc gtg gcc tac gga aac ctg gga cgc agc 211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
25 30 35
gtc gaa gag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259

```


Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	Asp	Leu	Val	Gly	Ile		
		40					45					50					
ttc	tgc	cac	cgg	gac	acc	ctc	gac	aca	aag	aag	cca	gtc	ttt	gar	gtc		397
Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val		
	55					60					65						
gac	gac	gtg	gac	aag	cac	gac	gac	gac	gtg	gac	gtg	cgc	ttc	ctg	tgc		395
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys		
	70				75					80					85		
atg	ggc	tac	gac	acc	gac	atc	cct	gag	cag	gca	cca	aag	ttc	gac	cac		403
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln		
				90				95					100				
ttc	gac	tac	acc	gta	gac	acc	cac	gac	aac	cac	cgc	gac	atc	cca	cac		461
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Asn		
			105					110					115				
cac	cgc	cag	gtc	atg	aac	gaa	gac	gac	acc	gca	gac	ggc	aac	gtt	gca		489
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala		
	120					125						130					
ctg	gtc	cct	acc	ggc	tgg	gat	cca	gga	atg	ttc	ccc	atc	aac	cgc	gtc		547
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val		
	135					140					145						
cac	gca	gag	gca	ttc	cca	gac	gag	cac	cag	cag	cac	acc	ttc	tgg	gac		585
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly		
	150				155					160					165		
cca	ggt	cgc	cca	cag	ggc	cac	ccc	gat	gct	tgg	cga	cgc	atc	cct	ggc		646
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly		
			170					175					180				
gtt	caa	aag	gca	ttc	cag	cac	acc	ctc	cca	ccc	gaa	gac	gac	ctc	gaa		691
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu		
		185						190					195				
aag	gac	cgc	cgc	ggc	gaa	gac	ggc	gac	ctt	acc	gga	aag	caa	acc	cac		739
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His		
	200						205					210					
aag	cgc	caa	tgc	ttc	gtg	gtt	gac	gac	ggc	gac	gat	cac	gag	cgc	atc		787
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile		
	215					220					225						
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	cac	ttc	gtt	ggc	tac	gaa	gtc		835
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val		
	230				235					240					245		
gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttc	gac	ccc	gag	cac	acc	ggc		883
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly		
		250						255						260			
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	ttc		931
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe		
		265						270					275				
aac	cac	acc	gtg	caa	tac	atc	ctc	aag	ctg	gac	cga	aac	cca	gat	ttc		979
Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	Arg	Asn	Pro	Asp	Phe		

280	285	290	
acc got too tca cag atc got ttc ggt cgc gca got cac cgc atg aag			1027
Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys			
295	300	305	
cag cag ggc caa agc gga got ttc acc gtc ctc gaa gtt got cca tac			1075
Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr			
310	315	320	325
ctg ctc too cca gag aac ttg gac gat ctg atc gca cgc gac ctc			1120
Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val			
330	335	340	
taatttagct cagaggggcaa gga			1143

<210> 40

<211> 140

<212> BRT

<213> Corynebacterium glutamicum

<400> 40

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu	
1 5 10 15	
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly	
20 25 30	
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met	
35 40 45	
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr	
50 55 60	
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp	
65 70 75 80	
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala	
85 90 95	
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His	
100 105 110	
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala	
115 120 125	
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe	
130 135 140	
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln	
145 150 155 160	
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu	
165 170 175	
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser	
180 185 190	
Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr	
195 200 205	

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 210 215 220
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 260 265 270
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
 275 280 285
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
 290 295 300
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
 305 310 315 320
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
 325 330 335
 Ala Arg Asp Val
 34

2210 41
 2211 353
 2212 DNA
 2213 Corynebacterium glutamicum

2214
 2215 CD3
 2216 (101)..(353)
 2217 PRXA10352

2200 41
 aatagatcag cgcacccgtg gtggaacaa aagggtcaac aatadgaaac gttcgtttc 60
 agtcttcatg aaagagatgt cctggaatca tcatctaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 3
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 11 15 20
 gcc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35
 gtc aaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50
 ttc tgc cgc cgg gcc acc ctc gac aca aag aag cca gtc ttt gat gtc 307
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
 55 60 65

gac gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc	355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys	
70 75 85	
atg gcc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcc cag	403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln	
90 95 100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc	451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg	
105 110 115	
cac gcc cag gtc atg aac gaa gcc gcc acc gca gcc gcc aac gtt gca	499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala	
120 125 130	
cag ttc tct acc gcc tgg gat cca gga atg ttc tcc atc aac gcc gtc	547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val	
135 140 145	
cac gcc gag cca ttc tta gcc gag cac cag cag cac acc ttc tgg gcc	595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly	
150 155 160 165	
cac agt ttc tca cag gcc cac tcc gat gct ttc cgc cgc atc cct gcc	643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly	
170 175 180	
gtt cac aag gca gtt cag tac acc cct cca tcc gaa gac gcc ctg gaa	691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu	
185 190 195	
atg gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc	739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His	
200 205 210 215	
atg gcc cca tgc ttc gtg gtt gcc gag ggc gcc gat cac gag gcc atc	787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile	
215 220 225	
gaa cac gac atc cgc acc atg cct gat tac ttc gtt gcc tac gaa gtc	835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val	
230 235 240 245	
gaa ttc acc ttc atc gac gaa gca acc ttc gac tcc gag cac acc gcc	883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly	
250 255 260	
atg cca cac ggt gcc cac gtg att acc acc gcc gac acc ggt gcc ttc	931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe	
265 270 275	
aac cac acc gtg gaa tac atc ctc aag	958
Asn His Thr Val Glu Tyr Ile Leu Lys	
280 285	

K210 - 42
 K211 - 286
 K212 - PRT

<213> Corynebacterium glutamicum

<1400> 42

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
 1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
 20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
 35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
 50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Gln Gln Ala
 85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
 100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
 115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
 130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Gln His Gln Gln
 145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 180 185 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
 275 280 285

<110> 43

<211> 1400

<212> DNA

<213> Corynebacterium glutamicum

<210>

<211> CDS

<212> (1)..(1377)

<213> EXA90972

<100> 43

ccg gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct	48
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala	
1 3 10 15	
acc gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat	96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn	
20 25 30	
gct gtg cgc cca gaa gac ggc gtt gtc acc gtc gct agt gtg cct ctg	144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu	
35 40 45	
ccg gac ctg ggt gaa gaa tac ggt acc cca ctg ttc gta gtc aac gag	192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu	
50 55 60	
gag gat ttc cgt tcc cgc cct cgt gac atg gct acc gca ttc cgt gga	240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly	
65 70 75 80	
ccc cgc aat gtt cac tac gaa cct aaa gaa ttc ctg acc aag acc att	288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile	
85 90 95	
gca cgt tgg gtt gat gaa gag ggt ctg gca ctg gac att gca tcc atc	336
Ala Arg Trp Val Asp Gln Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile	
100 105 110	
aac gaa ctg ggt att gcc ctg gct gct ggt ttc cca acc agc agt atc	384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile	
115 120 125	
acc ggc cac ggt aac aac aaa ggc gta gag ttc ctg cgc ggc ttg gtt	432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val	
130 135 140	
caa aac ggt gtt gga cac gtc ggt ctg gac tcc gca cag gaa cta gaa	480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu	
145 150 155 160	
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg	528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu	
165 170 175	
atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc	576
Ile Arg Val Lys Pro Gly Ile Gln Ala His Thr His Glu Phe Ile Ala	
180 185 190	
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc	624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser	
195 200 205	
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg	672

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu	
210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc	720
Val Gly Leu His Cys His Val Gly Ser Glu Val Phe Asp Ala Glu Gly	
225 230 235 240	
ttc aag ctg gca gga gaa ggc gtg ttc ggc ctg ttc tca cag atc cac	768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Glu Ile His	
245 250 255	
agc gaa ctg ggc gtt gcc att cct gaa ctg gat ttc ggt ggc gga tac	816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr	
260 265 270	
ggt att gcc tat acc gca gct gaa gaa cca ttc aac gtc gaa gaa gtt	864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val	
275 280 285	
gca tcc gac ctg ttc acc gca gtc gga aaa atg gca gcc gaa tta ggc	912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly	
290 295 300	
atc gac gca cca acc gtg att gtt gag cct ggc ggc gct atc gca ggc	960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly	
305 310 315 320	
gca tcc acc gtc acc atc taa gaa ttc ggc acc acc aaa gac ttc cac	1008
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His	
325 330 335	
gtc gac gac gcc aaa acc ggc ggt tcc atc gcc gtc gac gga ggc atc	1056
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met	
340 345 350	
tcc gac aac atc ggc cca gca ttc taa ggc tcc gaa taa gac gcc ggc	1104
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg	
355 360 365	
gtc gta tcc ccc ttc gcc gaa gga gac cca tta agc acc ggc atc gtc	1152
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val	
370 375 380	
agg tcc cac tcc gaa tcc ggc gat atc ctg atc aac gat gaa atc taa	1200
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr	
385 390 395 400	
ccn tat gac atc acc agc ggc gac ttc ctt gca ttc gca gcc acc ggc	1248
Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly	
405 410 415	
gca taa tgc taa gcc atg agc tcc ggc taa aac gcc ttc aca ggc ccc	1296
Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro	
420 425 430	
acc gtc gtg tcc gtc cgc gct ggc agc tcc ggc ttc atg ctg cgc cgc	1344
Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg	
435 440 445	
gaa acg ctg gac gac atc ctg tca cta gag gca taacgctttt cgaagcctga	1392
Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala	

450

455

ccc

1400

1210 - 44

1211 - 459

1212 - PRT

1213 - *Corynebacterium glutamicum*

1400 - 44

Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
1 5 10 15

Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
20 25 30

Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
165 170 175

Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
180 185 190

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
195 200 205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
210 215 220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
225 230 235 240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
245 250 255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
260 265 270

Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
 275 280 285
 Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
 290 295 300
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
 305 310 315 320
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
 325 330 335
 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340 345 350
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
 355 360 365
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
 370 375 380
 Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400
 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
 405 410 415
 Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
 420 425 430
 Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
 435 440 445
 Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
 450 455

#110: 45
 #111: 2121
 #112: DNA
 #113: Corynebacterium glutamicum

#120:
 #121: CDS
 #122: (101)..(2093)
 #123: EXA12653

#400: 45
 atcacagagtg ttagtgogtg gggcaggtct cactttcattc gacatcactc gagtatgctc 60
 atgggoggtta ttcattccaa taacccgcac agggaaaacta atg ata ccg aag ccc 115
 Met Ile Pro Lys Pro
 1 3
 gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tog gaa 163
 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
 10 15 20
 aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys

25	30	35	
gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa			259
Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu			
40	45	50	
egg gga atg ggg ggc aac tgg cgg gag ctg tac ccc agc atc gtg gaa			307
Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu			
55	60	65	
cga gct tcc tac gaa ggg ctt gac agc cta atc gga ttt gat cac tta			355
Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu			
70	75	80	85
goc egg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt			403
Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe			
90	95	100	
gaa tac ctc caa gaa ctc gta caa tcc aga gtg gta gac atc aac cac			451
Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His			
105	110	115	
ctg cat cgt ggc cgg gaa cca ctg aca gat tta gtt cgt gaa ctt gaa			499
Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu			
120	125	130	
ata act gtg ctg ata gac gct att ctt ccc ccg ccg gga gta gtg cca			547
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro			
135	140	145	
ggc aca ctg ctg cac aat tgg gta aaa caa gga tat gta aga atg agt			595
Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg			
150	155	160	165
ccc ggg aac egg ggg tta gat gta gcc ccc gac ggc acc gtt caa ggg			643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly			
170	175	180	
caa cga cat ttg gct gca gtc aga cgg atc aac gaa gat gtg gtt tcc			691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu			
185	190	195	
ggt aat gac aca ttg tgg cga tca tta cat gac ata atc ccg aag tgg			739
Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp			
200	205	210	
gct cgt cga gtt atc cgc gac cgc agc aac tat ccc gat agg gta cat			787
Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His			
215	220	225	
ggt act cca ccg ctt ccg gca cgg ttg caa ccc tgg cgc gaa aag ctc			835
Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu			
230	235	240	245
act tca gat ccg ggc aca tgc cgc cac ctg att gaa gaa ttc ggc agt			883
Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser			
250	255	260	
ccc gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag			931
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu			
265	270	275	

ttg gtt gac gcc ggc att caa atg ggg gtg gat act cga ata ttt ttt	979
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe	
280 285 290	
gcc cgc aaa ggc aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac	1027
Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp	
295 300 305	
acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg	1035
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val	
310 315 320 325	
ctt aat cgt gga gtc cca gga tag cgg atc att cta tcc gca got acc	1123
Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile	
330 335 340	
aaa ccg gac aga cta tgg gcc tta ggc atc gaa aat gcc gtg atc acc	1171
Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile	
345 350 355	
tct gtg gat tgg cgt cat gaa tta gat cgc att tgg gct tgg gtt ggt	1219
Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly	
360 365 370	
gac cgc gtt gca cca gtt gcc cct aga gta got cca gat cct gca gta	1267
Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val	
375 380 385	
tta cct cca act aga ttt ggt tag cgt gct gca gac tgg cgt aat cgg	1315
Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg	
390 395 400 405	
ctt acc gag gtg ata ccc ggt tgg gat att gta cgt ctt cag gta cag	1363
Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His	
410 415 420	
ctc cat gcc tat gct gca aaa gac cgt gct ctg gct ctg cag gaa tgt	1411
Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys	
425 430 435	
tgc caa ctc gtc gat cct ctc aga gaa tgc ggc cat tcc cca cag tat	1459
Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe	
440 445 450	
att gac ctt gga gga ggg ggg cct atg agc tac att gaa tct gag gaa	1507
Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu	
455 460 465	
gat tgg atc cgt tat cca tcc gct aaa tct ggc act tca gcc ggc tat	1555
Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr	
470 475 480 485	
gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg	1603
Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro	
490 495 500	
ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg ctt tct	1651
Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser	
505 510 515	

aag ggg gta got cag atg ctc att gac cgg gga ttg cgg tta cac ata 1639
 Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile
 520 525 530

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa 1747
 Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu
 535 540 545

ggt cct ttt gtg aaa arc cga agt gac ggg ttg cct cta gtg gga ctg 1795
 Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu
 550 555 560 565

ggt atg aac cga acc cag tgc cgg act aca tcc gat gat ttt ctc att 1843
 Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile
 570 575 580

ggt ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca 1891
 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
 585 590 595

tat cta gta ggt gcc tcc tgg atc gaa gat gag ctg att tta cgc cgg 1939
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg
 605 610

cga atc cga ttc cgg aca gga gtc aaa cca gga gat atc atc gga att 1987
 Arg Ile Asn Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
 615 620 625

ctt aat acc gca gga tcc ttt atg cat atc ttg gaa agt gca tcc cag 2035
 Phe Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
 630 635 640 645

cga atc cct ttg ggc aac aat gta gtc tgg cgg gag ggc cag tta gac 2083
 Glu Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
 650 655 660

gtt atc gat gag gat taagacataa caattcgcta atc 2121
 Asp Ile Asp Ala Asp
 665

C10: 46

C11: 666

C12: PRF

C13: Corynebacterium glutamicum

C100: 46

Met Ile Pro Lys Pro Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu
 1 5 10 15

Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu
 20 25 30

Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
 35 40 45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
 50 55 60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
 65 70 75 80

Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
 85 90 95
 Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
 100 105 110
 Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
 115 120 125
 Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
 130 135 140
 Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
 145 150 155 160
 Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
 165 170 175
 Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr
 180 185 190
 Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp
 195 200 205
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
 210 215 220
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
 225 230 235 240
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
 245 250 255
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
 260 265 270
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
 275 280 285
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
 290 295 300
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
 305 310 315 320
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
 325 330 335
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
 340 345 350
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
 355 360 365
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
 370 375 380
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
 385 390 395 400

Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
 405 410 415
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu
 420 425 430
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly
 435 440 445
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
 450 455 460
 Ile Gln Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala
 465 470 475 480
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu
 485 490 495
 Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu
 500 505 510
 Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly
 515 520 525
 Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly
 530 535 540
 Val Thr Leu Ala Glu Val Ala Pro Val Lys Thr Arg Ser Asp Gly Leu
 545 550 555 560
 Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser
 565 570 575
 Arg Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly
 580 585 590
 Ala Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu
 595 600 605
 Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly
 610 615 620
 Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu
 625 630 635 640
 Leu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro
 645 650 655
 Gln Gly Gln Leu Asp Asp Ile Asp Ala Asp
 660 665

4210 - 47

4211 - 893

4212 - DNA

4213 - *Corynebacterium glutamicum*

4216 -

4217 - CDS

4218 - (101)...(970)

4219 - EXA01393

<400> 17

caaaagcaqa cctgtaatga agatttccat gatcaccatc gtgacctatg gaagtaactta 60
 agtaaaatga ttgggttctta acatgggtta atatagcttc atg aac ccc att caa 115
 Met Asn Pro Ile Gln
 1 5

ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163
 Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala
 10 15 20

tcc tta gcc ctt tcc att tcc ccc tgg ggg gtg agt cag cgc gtt aaa 211
 Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
 25 30 35

gct ctg gag cat cac gtg ggt cga gtg ttg gta tgg cgc acc caa cgg 259
 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
 40 45 50

gcc aac gca acc gaa ggc ggt gaa ctg ctt gtg caa gca ggc cgg aaa 307
 Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
 55 60 65

atg gta ttg ctg caa gca gaa act aac ggc caa cta tcc gga cgc ctt 355
 Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu
 70 75 80 85

gct gaa atc cgg tta acc atc gcc atc aac gca gat tgg cta tcc aca 403
 Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr
 90 95 100

tgg ttt act ccc gtg ttc aac gag tta gct tct tgg ggt gga gca acc 451
 Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr
 105 110 115

ctc acg ctg cgc ttg gaa gat gaa tcc cac aca tta tcc ttg ctg cgg 499
 Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg
 120 125 130

cgt gga gat gtt tta gga ggc gta acc cgt gaa gct aat ccc gtg ggc 547
 Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala
 135 140 145

gga tct gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca 595
 Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
 150 155 160 165

acc ccc tca ttg cgg gat gcc cac atg gtt gat ggg aaa cta gat tgg 643
 Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp
 170 175 180

gct ggc atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691
 Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
 185 190 195

cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739
 Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val
 200 205 210

tcc att gtc cgg tgg ggc gaa ggt ttt ggt gag gca att cgc cga ggc 787

Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly
 215 220 225

ctt ggt tgg aga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa 935
 Leu Gly Trp Gly Leu Leu Pro Gln Thr Gln Ala Ala Pro Met Leu Lys
 230 235 240 245

gca gga gaa gtg atc ctc ctg gat gag ata ccc att gag aca cgg atg 883
 Ala Gly Glu Val Ile Leu Leu Asp Gln Ile Pro Ile Asp Thr Pro Met
 250 255 260

tat tgg caa aga tgg cgg ctg gaa tct aga tct cta gct aga ctc aca 931
 Tyr Trp Gln Arg Trp Arg Leu Gln Ser Arg Ser Leu Ala Arg Leu Thr
 265 270 275

gac ccc gtc att gat gca gca atc gag gga tgg cgg cct tagttacttc 980
 Asp Ala Val Val Asp Ala Ala Ile Gln Gly Leu Arg Pro
 280 285 290

tgaaaagggtt cag 993

<210> 42
 <211> 290
 <212> PRT
 <213> Corynebacterium glutamicum

<110> 16
 Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Gln Gly
 1 10 15

Ser Phe Gln Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
 20 25 30

Ser Gln Arg Val Lys Ala Leu Gln His His Val Gly Arg Val Leu Val
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Gln Val Ala Ser
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Pro Gly Glu
210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Gln Ser Arg Ser
260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
275 280 285

Arg Pro
290

<210> 49
 <211> 1626
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (131)...(1695)
 <223> EXA03241

<400> 49
 ggtcttcagc ctctctaaac aattcatctg cacttgatta attggccca agattacgcg 60

aaqthtagcg aattcgccgt aagtcaccta cgttaaata gtc aat acr caa tca 115
 Val Asn Thr Gln Ser
 1 5

gat tct ggc ggg tct caa ggt gca ggc gcc aca agt cgt act gta tct 163
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
 10 15 20

att aga acc ctg atc ggc ctg atc atc gga tog acc gtc ggc gcc gga 211
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
 25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc ggc 259
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
 40 45 50

atg ctg atc ggc tgg ctg atc gcc ggt gtc ggc atg ttg tcc gta gcc 307
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
 55 60 65

ttc gtg ttc cat gtt att gcc cgc cgt aaa cct cac ctg gat tct ggc 355
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
 70 75 80 85

gtc tac gca tat ggc cgt gtt gga ttg ggc gat tat gta ggt ttc tcc	403
Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser	
90 95 100	
ccc gct tgg ggt tat tgg ctg ggt tca gtc atc ggc caa gtt ggc tac	411
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr	
105 110 115	
gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc	429
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser	
120 125 130	
caa gat cat caa ttt gtc tca ggc ttg gca gtt agc gct tgc acc tgg	547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp	
135 140 145	
ctg ctg ttt gca gtt gtt tcc cga gga att agc caa gct cat ttc ctg	585
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu	
150 155 160 165	
aca acg gtc acc acc ctg gcc aac att ctg cat ctg ttg tgc ttc atc	643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Lys Phe Ile	
170 175 180	
atc att gtt caa ttc ttg gcc ttt agc tgg gag aag ttc cat gtt gat	681
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
tta tgg ggc cgt cat gct gcc gtc ggc agc att ttt gat acg gtc cgc	739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp His Val Arg	
200 205 210	
ggc atc atg ttc tac acc gtt tgg ctg ttc atc ggt att caa ggt gca	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile His Gly Ala	
215 220 225	
tgg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cgc gat	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gtc att cgt ttt ctg gct gtt ttc att ttg ctg ctg ttg att cat	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Val Ser Ile Ser	
250 255 260	
tgg ctg agc ttc ggt gta ctg acc caa caa gag ctg gct ggc tta caa	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atc ggc tgg gty ttc gaa gct att gtt ggt tca tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
280 285 290	
gac gca ttg att tgg ttg gct ctg tgt ctt ttg gtt ctt ggc gcc tat	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr	
295 300 305	
gtg tcc tgg caa atg ctg tgc gca gaa caa ctg ggc ttg atg gca atg	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
310 315 320 325	

gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt got 1123
 Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
 330 335 340
 ggc tgg atg got cag ctg atc tcc acc atc gtg att cag att ttc atc 1171
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
 345 350 355
 atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg 1219
 Ile Ile Phe Phe Leu Asn Gln Thr Thr Tyr Val Ser Met Val Gln Leu
 360 365 370
 got acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg 1267
 Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
 375 380 385
 gtc ctg ctg gca aca cgt gga aaa gga atc acc cac cca tat gcc ggc 1315
 Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
 390 395 400 405
 acc cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc 1363
 Thr Arg Phe Asp Asp Ser Gly Pro Gln Ile Ser Arg Arg Gln Asn Arg
 410 415 420
 acc cac ctc atc gtc ggt tta gta gca acc gtg tat tta gtg tgg ctg 1411
 Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
 425 430 435
 ttt tac got gca gaa cgc cag ttt gta ctc ttc gga gcc atg gcc atg 1459
 Phe Tyr Ala Ala Gln Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
 440 445 450
 gtt acc gcc tta atc ccc tac gtg tgg acc agg att tat cgt gcc gaa 1507
 Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Gln
 455 460 465
 cag gtg ttt aac cgc ttt gaa atc gcc gtg gtt gtt gtc ctg gtc gtt 1555
 Gln Val Phe Asn Arg Phe Gln Ile Gly Val Val Val Val Leu Val Val
 470 475 480 485
 got gcc agc gcc gcc gtt att ggt ttg gtc aac gga tca cta tgg ctt 1603
 Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
 490 495 500
 taacacacga aaccttcctg cta 1626

4110 - 30

4111 - 501

4112 - PRT

4113 - *Corynebacterium glutamicum*

4420 - 30

Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
1 10 15

Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
 50 55 60
 Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
 65 70 75 80
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
 85 90 95
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
 100 105 110
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
 115 120 125
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
 130 135 14
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
 145 150 155 160
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
 165 170 175
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu
 180 185 190
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
 195 200 205
 Phe Asp Gln Val Asp Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
 210 215 22
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
 225 230 235 240
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
 245 250 255
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
 260 265 270
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
 275 280 285
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
 290 295 300
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
 305 310 315 320
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
 325 330 335
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
 340 345 350
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
 355 360 365

Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
270 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr
335 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser
405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg
450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
485 490 495

Gly Ser Leu Ser Leu
500

<210> = 51

<211> = 122

<212> = DNA

<213> = Corynebacterium glutamicum

<220> =

<221> = CDS

<222> = (101)...(999)

<223> = RXA01394

<400> = 51

gaacaaagtg tccagttgaa tgggggttcac gaagctatat caaacatgt taagaaccaa 60

ccatttact taagtaacttc cataggtcac gatggtgac atc gaa atc ttc att 115
Met Glu Ile Phe Ile
1 5

aca ggt ctg att ttg ggg gcc agt ctt tta ccg tcc atc gga ccg gag 163
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctg att gag 211
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
25 30 35

gcc att ctg ggc tgt tta att tct gac gtc ttc ctg ttc atc gcc ggc 259
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
40 45 50

acc ttg ggc gtt gat att ttg tcc aat gcc ggc ccg atc gtg ctg gat 307
Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70 75 80 85
 gca ggc aaa gac gcc atg aca aac aag gtg gaa ggc aca cag atc att 403
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
 90 95 100
 gaa gaa aca gaa aca aac gtg aac gat gac aag cct ttg ggc ggt tgg 451
 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
 105 110 115
 ggc ttg gcc aat gac aag cgc aac cgg gtg cgg gtg aag gtg aag gtc 499
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
 120 125 130
 gat aag cag cgg gtt tgg gta aag aac atg ttg atg gca atc gtg ctg 547
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
 135 140 145
 aac tgg ttg aat cgg aat ggc tat ttg gac ggc ttt gtg ttt atc ggc 595
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
 150 155 160 165
 ggc atc gcc ggc ggc aca tac ggc gac aac gga cgg tgg att ttc gcc gct 643
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
 170 175 180
 ggc cgg ttc ggc gca aac cgg atc atc ttg ttc cgg atg atg ggt ttc gcc 691
 Gly Ala Phe Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
 185 190 195
 gca gca gca ttg aca cgc cgg atg aac aag aac aag atg tgg cgc tgg 739
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
 200 205 210
 atc aac gtc gtc gtg gca gtt gtg atg aac gca ttg gcc atc aac ctg 787
 Ile Asn Val Val Val Ala Val Met Thr Ala Leu Ala Ile Lys Leu
 215 220 225
 atg atg atg ggt tagttttcgc gggttttgga atc 822
 Met Leu Met Gly
 230

110 - 52

111 - 233

112 - PBT

113 - *Corynebacterium glutamicum*

1400 - 12

Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
 1 5 10 15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
 20 25 30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
 35 40 45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala

gaa gtc gog got tat ttg gtt gat aag ggc ttg gat tot ttg gtt ctc	259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu	
40 45 50	
gog ggc aac aat ggt gaa tcc caa acg aca acc ggc got gaa aaa cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctc aag ggc gtt cgt gag gaa gtt ggg gat cgg gog aag ctc	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
acc ggc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctc gog	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa got got got cct got cgc gca gac ggc ctt tca gtt gta att cct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
105 110 115	
tat tac tcc aag ccc agc caa gag gga ttg ctg gog aac ttc ggt gca	499
Tyr Tyr Ser Lys Pro Ser Glu Glu Gly Leu Leu Ala His Phe Gly Ala	
120 125 130	
acc got gca gca aac gag gtt caa att tgn ctc tar gac att cct ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
135 140 145	
cgg tca ggt att caa att gag tct gat aac atg aga cgc ctg aat gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160 165	
tca cct acg att ccc ggc ctg aag gac gca aag ggt aac ctc gtt gca	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
170 175 180	
goc aag tca ttg att aaa gaa aag gga ctt ggc tgg tat tca gac gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
gac caa cta aac ctt gtt tgg ctt got ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gca gcc ccc aca gca tca cgt gag ttg tcc aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt ggc cgg gaa atc aac ggc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca ccg ctg gta got gcc caa ggt cgc ttg ggt gga gtc aac ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gca aaa got got ctg cgt ctg cag gcc atc aac gta gga gat cct cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 270 275	
ctt caa att atg got cca aat gag cat gaa ctt gag got ctc cga gaa	979

Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
 280 285 290

gac atg aaa aaa gct gga gtt ata taaatatgaa tgattccaga aat 1026
 Asp Met Lys Lys Ala Gly Val Leu
 295 300

<210> 34

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<240> 34

Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr
 1 5 10 15

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
 2 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
 50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
 85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
 10 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Glu Glu Gly Leu Leu
 115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
 130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
 145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
 165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
 180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
 195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
 210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
 225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
 245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
261 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
290 295 300

<210> : 65

<211> : 1071

<212> : DNA

<213> : Corynebacterium glutamicum

<210> :

<211> : CDS

<212> : (101)..(1048)

<213> : EXS92021

<210> : 65

tttggttggc gaggagatct aatcctggtt tgagttcaga gtacacaggt ttaagcctac 60

aaaccttagt taaaacatga tggagcgggt cgattaaaa atg agt gaa aac att 115
Met Ser Glu Asn Ile
1 5

cgc gga gcc caa gaa gtt gga atc gaa aat att gcc atg gac ggg aac 163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
10 15 20

atc ctg gac cgc tgg tac caa gaa ccc caa att ctg aac cgc gat cag 211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
25 30 35

tgc gct gaa cgc tac caa tgg gaa gtg ggc aac aca cgc ctg gga gaa 259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
40 45 50

aac gaa ctg aac caa cgg atg ctg cag ttg gta aaa ctg gac caa gat 307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
55 60 65

cgc ctg gtc gaa cag gta gaa gtc cgc aac gtt atc ccc gat ctg ccc 355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
70 75 80 85

caa cct caa gta gac cgc cag gat gtt tac ctg cgc ctg cag ctg ctt 403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
90 95 100

ccc cac cgg ctg gtc cgc ccc cag gaa atg cac atg caa aac aac ttg 451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
105 110 115

gag ctg ctg ccc gac gtg gtg ttg aca aac aag ggc cct tgc ctt cct 499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
120 125 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctg atc 547

Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
 135 140 145
 cac gtc tac tgt gtg gac ggt ttt ccc cgc atg gtc gac tat gtg gtc 595
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165
 ccc ccc gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180
 tac att gct ccc ggt acc tat gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195
 acc tcc gcc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210
 ggt gtc gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225
 cag tcc ccc aga gat gaa cag cgc cgc cgt ttg cag ttg agc atc ggc 835
 Glu Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245
 caa aac tcc aac ttt ggt gtc agc tcc gga atc atc gga ctg agt ctg 883
 Glu Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260
 pra gac aat tgc cac atc gga aat aac att gtt ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275
 acc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290
 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305
 caa ttt gcc cgc ctg aaa gct agaccattt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

0210 - 16

0211 - 316

0212 - PFT

0213 - *Corynebacterium glutamicum*

0400 - 56

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

<222> (191)..(1273)

<223> EX302157

<400> 57

gggtagaatt ggcacgatgg tgetgcggga tgtttttgat cgggagaatt atcctgaagg 60

caccccttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
Met Ser Thr Leu Glu
1 5

aat tgg cca cag gtc att att aat agc tac ggc acc cca cca gtc gag 163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
10 15 20

ctg gtc tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
25 30 35

tac atc gac ttg ctg ggc ggc atc gca gtc aac ggc ttg ggc cag ggc 259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
40 45 5

cac tgg ggc atc atc gag ggc gtc acc aac cag atc ggc caa ctt ggt 307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
55 60 65

cac atc tca aac ttg ttc gca tcc agc cca gtc gtc gag gtc ggc gag 355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu
70 75 80 85

gac ttc atc aag cgt ttt tcc gtc gtc ggc acc ctg ggc ggc cca 403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
90 95 100

aac tgg gtc ttc ttc tgc aac tcc ggc ggc gaa gca aac gac gtc gtc 451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Gln Ala Ala
105 110 115

tac tag att gca cgc ttg act ggt cgt tcc cgg att ctg gtc gca gtc 499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
120 125 130

cac ggt ttc cag ggc cgc acc atg ggt tcc ctg ggc ctg act ggc cag 547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
135 140 145

cca gac aag cgt gaa ggc ttc ctg cca atg cca agc ggt gtc gag ttc 595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gag acc aac 643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Gln Thr Asn
170 175 180

cca acg gat gtc got got atc ttc ctg gag cca atc cag ggt gaa acc 691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
185 190 195

ggc gtt gtt cca gca cct gaa gga ttc ctg aag gca gtc cgc gag ctg 739
Gly Val Val Pro Ala Pro Gln Gly Phe Leu Lys Ala Val Arg Glu Leu
200 205 210

ttg gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
 215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245

ccc tat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260

agt gat tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290

aag caa gtg cag tat gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305

ccc aag ggc gag ctc ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325

gaa cac gtc ctt ggc agg ggc ttg atg ttg ggc ggc ggc ctc gag cgc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340

tcc ttc gca aag caa gct ctt ctt gat ggt ttc aag cac ggc gtt att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355

ttg aat gca cag ggc gar aac att atc cgt ttg acc ccc ccc ctc gtc 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370

ttc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag acc 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385

ttc gcc taaaggacac aaacttatga ctt 1296
 Ile Ala
 390

0110-58

0111-391

0112-FRT

0113-Corynebacterium glutamicum

0400-58

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Glu Gly Glu Thr Gly Val Val Pro Ala Pro Gln Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350

Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
355 360 365

Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
370 375 380

Ala Ile Ala Glu Thr Ile Ala
385 390

#210 - 19

#211 - 1008

#212 - DNA

#213 - *Corynebacterium glutamicum*

#220 -

#221 - CDF

#222 - (151)...(985)

#223 - EX000733

#100 - 19

aggaggaggt tgcgggtatt ggaaagcaca cgaatttgc gaacacgtgc ggtacctacc 60

gggaattgt tgaatcccaa gagactggcg agggcgcaatc atg agt aat act gaa 115
Met Ser Asn Thr Ala
1 5

ggc tcc cgc ggg cgt tcc cat cag gca gac gcc ggc ccg aat caa aag 163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
10 15 20

aca ccc aat ttc gga cca tat gcc aac agg ctt ttc gga att cta gcc 211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly
25 30 35

cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc 259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser
40 45 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn
55 60 65

gtg ttg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt ggc tca 355
Val Val Phe Gln Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser
70 75 80 85

aag gaa gat atc atc gcc cag ttg cag gct gca ggt aaa cat aat cag 403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln
90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca ggc tca ggc att gat 451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp
105 110 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
120 125 130

atc ggt agc ctg ttg tgc ttg ttc cag gcc cgg atg ctc aac cgc atc 547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile

135	140	145	
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc			595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile			
150	155	160	165
cac cgg cta cgg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg			643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu			
	170	175	180
ttt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa			691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln			
	185	190	195
aaa acc ttg tta cag gcc atc act tcc cta ctg acc gtc atc ggt gtg			739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val			
	200	205	210
ttc ctg atg atg ttt atc atc tcc cca ctg ctg gca ctg gtg gcc ctg			787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu			
	215	220	225
tta tcc att cgg gtc acc atc gtg gtc act gtg gtg gtt gcc acc cgt			835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg			
	230	235	240
taa cag ata ctc ttt gcc gaa cag tgc aag cag acc ggt att ttg aat			883
Ser Gln Lys Leu Phe Ala Gln Gln Trp Lys Gln Thr Gly Ile Leu Asn			
	245	250	255
ccg cgg ctg gag gaa acc tac tct gcc cac gcc gtg gtt aag gtt ttc			931
Ala Arg Leu Gln Gln Thr Tyr Ser Gly His Ala Val Val Lys Val Phe			
	260	265	270
gga cac cca aag aat gtt caa gaa gaa ttc gag gaa gaa aat caa ggt			979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala			
	275	280	285
tgt cta taaggccagc ttctgttccc agt			1008
Cys Val			
	290		

*210: 60

*211: 396

*212: 357

*213: *Corynebacterium glutamicum*

*400: 60

Met	Ser	Asn	Thr	Ala	Gly	Pro	Arg	Gly	Arg	Ser	His	Gln	Ala	Asp	Ala
1				3				10					15		

Ala	Pro	Asn	Gln	Lys	Ala	Gln	Asn	Phe	Gly	Pro	Ser	Ala	Lys	Arg	Leu
			10					25					30		

Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe
		35					40					45			

Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu
	50					55					60				

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
 65 70 75 80
 Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
 85 90 95
 Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
 100 105 110
 Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
 115 120 125
 Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg
 130 135 140
 Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu
 145 150 155 160
 Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile
 165 170 175
 Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile
 180 185 190
 Lys Glu Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu
 195 200 205
 Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu
 210 215 220
 Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val
 225 230 235 240
 Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln
 245 250 255
 Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala
 260 265 270
 Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu
 275 280 285
 Gly Glu Asn Gln Ala Cys Val
 290 295

3110 - 61
 3111 - 426
 3112 - DNA
 3113 - Corynebacterium glutamicum

3120 -
 3121 - CDS
 3122 - (1) .. (426)
 3123 - RXC00861

410 - 61
 agt gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48
 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

cct atg gct ggc ctg tct cgc atg ggc cgt cgt gag cac cga cag atc 96
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

ggt aac gaa gaa gca atg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

ggt cca act gtt gtt aac ggt cgc gac gcc aag gtc cac aac tgc ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

aac cgc tac tcc gga cag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

aac aac gct atg cct atc cac gcc cag tgg ccc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

aag caa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtc ctt 384
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

gta caa aac ggt gtt ctg gtt gat atg gtc aac ggt cgc gca 426
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

< 10 - 62
 < 11 - 142
 < 12 - PRT
 < 13 - *Corynebacterium glutamicum*

< 100 - 62
 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 10 15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

Phe Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu

[illegible]

150	155	160	165	
atc tgt cgc aac atg acc gty ttt gag tac aac aac cgt ctg ctc atc				643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile				
	170	175	180	
gtg aac tgt ggt gtc ctc ttc cca tct tca ggt gag cca ggc gtt gac				691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp				
	185	190	195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc				739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val				
	200	205	210	
gat cca ttg gtc gtt act cac gga cac gaa gac cac att ggt gct att				787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile				
	215	220	225	
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt				835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg				
	230	235	240	245
ttc acg ttg gat ctg att gca gct aag tgt aag gaa cac cgt cag cgt				883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg				
	250	255	260	
ccg aag ctg atc gag gtc aac gag cag tcc att gag gac cgc gga ccg				931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro				
	265	270	275	
ttc acg att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt				979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu				
	280	285	290	
ggc att gct atc aag act cct gct ggt ttg ctc atc cac acc ggt gac				1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp				
	295	300	305	
atc aag ctg gat cag act cct cct gat gga cgc cca act				1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr				
	310	315	320	

*210 - 64

*211 - 122

*212 - ERT

*213 - *Corynebacterium glutamicum*

*410 - 64

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1					5				10					15	

Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20					25					30			

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35				40					45				

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55				60					

Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
 65 70 75 80
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
 85 90 95
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
 100 105 110
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160
 Gly Gly Ile Ser Gln Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190
 Gln Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
 245 250 255
 Gln His Arg Gln Arg Pro Lys Leu Ile Gln Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
 305 310 315 320
 Pro Thr

<210 - 65
 <211 - 1547
 <212 - DNA
 <213 - Corynebacterium glutamicum
 <214 -
 <215 - CD1
 <216 - (101...1594)
 <223 - EXC02095

<400> 65

ctctctttgggt cctctcctcca cccatttttta agtactcaag acccttcctcaa cagaaaggat 60

tactcctcca acaggtctcaa aaatactgaa aggetcaccg atg aaa act gag caa 115
Met Lys Thr Glu Gln
1 5

tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag caa caa 163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
10 15 20

cgc atc cgc caa ctt att tcc gtg ggc tgg cag cga cct tgg ctg acc 211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
25 30 35

tca ttc acc gta atc agc gct tta gct gca aag ttg ttt gaa ctt aca 259
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr
40 45 50

ctt cct ctt ttg acc ggt ggc gcc atc gat atc ggc ctg gga aat acc 307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asp Thr
55 60 65

gga cat act tta acc act gac ctg ctg gac cag ttc act ccg agt gga 355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly
70 75 80 85

tta agc gag ttg acc agc gtc att gcc ctt atc gtg ctg ctg ggc ttg 403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu
90 95 100

ctt agc ctt gcc agt caa ttt gga cgg cga ttc acc gca ggc aag ctg 451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu
105 110 115

agc atg gag tta cag cat gat gtc cgg ctt aaa acc atg cgc tca ttg 499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu
120 125 130

cag aac ctg cat ggg caa ggt cag gac tct att cgc aca ggc caa gta 547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val
135 140 145

gtc agt cgc tcc att tgg gat atc aac atg gtg caa agc ctt gtg ggc 595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala
150 155 160 165

atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctg aat ttg 643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu
170 175 180

gtg atc atg ctg gct att tcc ccg ccg ctg aac atc atc atc gct gca gtg 691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val
185 190 195

ttg gtg cct ttg ctg ttg ttg gcc gtg gcc tat tgg cga aaa ggc ctt 739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu
200 205 210

ttt ggc tcc acg tgg tgg gcc cag caa aag gct ggc gat ctg acc act 787

Phe	Ala	Ser	Thr	Trp	Ser	Ala	Gln	Gln	Lys	Ala	Ala	Asp	Leu	Thr	Thr		
315						220				225							
cat	gtg	gaa	gaa	act	gtc	acc	ggg	atc	ggc	gtg	gtc	aag	gca	ttt	ggg	835	
His	Val	Glu	Glu	Thr	Val	Thr	Gly	Ile	Arg	Val	Val	Lys	Ala	Phe	Ala		
330					335				340					245			
cag	gaa	gac	ggc	gag	acc	gac	aaa	ttg	gat	ctc	acc	gca	cgt	gag	tta	883	
Gln	Glu	Asp	Arg	Glu	Thr	Asp	Lys	Leu	Asp	Leu	Thr	Ala	Arg	Glu	Leu		
				250				255						260			
ttt	ggc	cag	ggc	atg	ggc	act	gaa	cgt	ctg	acc	gca	aag	ttc	ctc	ggc	931	
Phe	Ala	Gln	Arg	Met	Arg	Thr	Ala	Arg	Leu	Thr	Ala	Lys	Phe	Ile	Pro		
			265					270					275				
atg	gtt	cag	cag	ttt	ggc	cag	ttt	gct	ttg	gtg	ctc	aag	att	gtt	ggc	979	
Met	Val	Glu	Gln	Leu	Pro	Gln	Leu	Ala	Leu	Val	Val	Asn	Ile	Val	Gly		
		311					285					290					
ggg	ggc	tat	ttg	ggc	atg	act	ggg	cac	atc	acc	gtg	gac	acc	ttt	gtg	1027	
Gly	Gly	Lys	Leu	Ala	Met	Thr	Gly	His	Ile	Thr	Val	Gly	Thr	Phe	Val		
	295				300						305						
ggg	ttt	tat	acc	tat	ctc	act	aga	ttg	ttg	ggg	gtg	ggt	agg	acc	gtg	1075	
Ala	Phe	Ser	Ser	Tyr	Leu	Thr	Ser	Leu	Ser	Ala	Val	Ala	Arg	Ser	Leu		
310					315					320					325		
ggg	ggc	atg	ctc	atg	ggc	gtg	ttg	ttg	ggg	gtg	tct	tat	gtg	cag	ggc	1123	
Ser	Gly	Met	Leu	Met	Arg	Val	Gln	Leu	Ala	Leu	Ser	Ser	Val	Ile	Arg		
				330				335						340			
ttt	ttt	gaa	gac	ttt	tat	ttt	cag	cct	gaa	agg	acc	gat	cct	gca	cac	1171	
Ile	Phe	Gln	Val	Ile	Asp	Leu	Gln	Pro	Gln	Arg	Thr	Asp	Pro	Ala	His		
		345					350						355				
acc	gtg	tca	ttt	ggc	gac	act	acc	gtg	ggg	gtg	ttg	ttc	acc	acc	gta	1219	
Pro	Leu	Ser	Leu	Pro	Asp	Thr	Pro	Leu	Gly	Leu	Ser	Phe	Asn	Asn	Val		
		360					365					370					
gat	ttc	cgt	ggg	att	ctc	aac	ggg	ttt	cag	gtg	ggg	gtt	cag	acc	ggg	1267	
Asp	Phe	Arg	Gly	Ile	Leu	Asn	Gly	Phe	Gln	Leu	Gly	Val	Gln	Ala	Gly		
	375					380					385						
gaa	acc	gtt	gtg	ttg	gtg	ggc	cct	cga	ggg	tca	agg	acc	atg	ggt		1315	
Gln	Thr	Val	Val	Leu	Val	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	Met	Ala		
390					395				400					405			
gtg	cag	ctt	ggt	ggg	aac	ttt	tat	cga	cga	gac	agg	ggg	cac	atc	ggc	1363	
Val	Gln	Leu	Ala	Gly	Asn	Phe	Tyr	Gln	Pro	Asp	Ser	Gly	His	Ile	Ala		
				410				415						420			
ttt	gat	agg	aac	ggc	cac	ggc	act	ggc	ttc	gac	cac	ctc	acc	cac	agg	1411	
Phe	Asp	Ser	Asn	Gly	His	Arg	Thr	Arg	Phe	Asp	Asp	Leu	Thr	His	Ser		
			425					430					435				
gat	atc	ggc	agg	aac	ctc	atc	ggg	gtt	ttt	gat	cag	cag	ttc	ttg	tac	1459	
Asp	Ile	Arg	Arg	Asn	Leu	Ile	Ala	Val	Phe	Asp	Glu	Pro	Phe	Leu	Tyr		
			440				445					450					
tcc	tcc	tcc	ata	cgg	cga	gaa	cac	ctc	gat	ggg	ttt	gga	tgt	cag		1504	
Ser	Ser	Ser	Ile	Pro	Arg	Glu	His	Leu	Asp	Gly	Phe	Gly	Cys	Gln			

455 460 465
 tgatgagcaq atcgaacacg cag 1527

02100: 66
 02110: 468
 02120: PRT
 02130: Corynebacterium glutamicum

04000: 66
 Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala
 1 5 10 15
 Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
 20 25 30
 Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45
 Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60
 Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Leu
 85 90 95
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
 145 150 155 160
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
 165 170 175
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
 180 185 190
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
 195 200 205
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
 210 215 220
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
 225 230 235 240
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
 245 250 255
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
 260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
 325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
 340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
 355 360 365

Ser Pro Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
 370 375 380

Gly Val Gln Ala Gly Gln Thr Val Val Leu Val Gly Pro Pro Gly Ser
 385 390 395 400

Gly Gly Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
 435 440 445

His Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Gln His Leu Asp Gly
 450 455 460

Phe Gly Cys Gln
 465

<110> 67
 <110> 195
 <110> DNA
 <110> Corynebacterium glutamicum

<110>
 <110> CDS
 <110> (14) .. (272)
 <110> EX003135

<110>
 <110> misc_feature
 <110> 67
 <110> n = a, c, t, or g

<110> 67
 agcgcccaac cgttcagacc agcggtttct ctgaggatgc aaagtccatg atgggtnagg 60
 tcaactgagct gtccgaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113
 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn

	1	5	10	
gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc				161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe				
	15	20	25	
gtc cag cag aag tgg aag cgc cag cag gtc atc atg cca acc gtc att				209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile				
	30	35	40	
cgc atg act gag gaa acc acg cac atc ggt gac gat gag gtt cgc gct				257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala				
	45	50	55	
cca cgc gag tcc ctg taaaagcatt tcgttttttcg acg				295
Ser Arg Glu Ser Leu				
	60			

110 - 48
 111 - 48
 112 - ERF
 113 - Corynebacterium glutamicum

Met Asp Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val				
1	5	10	15	
Trp Glu Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys				
20	25	30		
Arg Glu Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr				
35	40	45		
Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu				
50	55	60		

114 - 68
 115 - 1171
 116 - DNA
 117 - Corynebacterium glutamicum

118
 119 - 073
 120 - (101)...(1147)
 121 - EXA00115

tgattctcg agtctgtaca ccttgatca aagcccgagt gttccgtaga ttaactttgt	60
gtatattgt gaactacacc ccatactggt aggagttttc atg ctc gac aat agt	115
	Met Leu Asp Asn Ser
	1 5
ttt tac acc gca gag gtt cag gcc cca tac gaa acc gct tcc att ggc	163
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly	
	10 15 20
agg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct	211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala	

25	30	35	
tac gct aca gct gga aag ctc aac gag gag aag tcc aac gcc atc ctc Tyr Ala Thr Ala Gly Thr Leu Asn Gln Asp Lys Ser Asn Ala Ile Leu 40 45 50			259
att cgg aag tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr 55 60 65			307
atc ggc act gat cat ggc ctc gat cca tca aag tat ttc atc atc tcc Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser 70 75 80			355
atc aac caa att ggt aat ggt tgg tgg atc tcc cat gcc aac acg gat Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala 85 90 95 100			403
gat gag agc atc tcc aag tcc aag ttc cag aat gtt cgc att ggt gat Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp 105 110 115			451
gat gtc gtt gat cag gag cgc ctc ttc agc caa gag ttt ggt att acc Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Gln Phe Gly Ile Thr 120 125 130			499
gag ctc ttc gct gtc gtt agt gat tcc aag ggt gag cag caa acc tat Gln Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr 135 140 145			547
gag tgg att gtt cgc ttc cat gag caa ttc cat cgc gca gct cgg atc Gln Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile 150 155 160 165			595
ggc gcc act cgg aac aac act cat cat ttc atc ttc acc cag act Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr 170 175 180			643
ctt aat gag acc gtt gag gcc gat cca ggc ttc aat ggc gcc gaa tac Leu Asn Gln Thr Val Gln Ala Asp Pro Gly Phe Asn Gly Gly Gln Tyr 185 190 195			691
tcc tcc cat gag gag gta gcc gat gga att cgc cgt caa tcc cat ctt Ser Ser His Gln Gln Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu 200 205 210			739
tgg gat gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Gln Ala Trp 215 220 225			787
cgt cgc ctc gga ctt gaa agt aag gag tca gtc ctc gcc gag ttc ctc Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu 230 235 240 245			835
gat cgg ctc ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala 250 255 260			883
tgg aag tgg cag cat gcc gat gtc tct cgc cac acc gcc gcc gag ttg Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu 265 270 275			931

gca gag got ott ggc cga gtg aag got aag acc ttc gtt atg ccc atc 979
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
 230 235 290
 ago gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
 295 300 305
 ctg atc cca ggc agc gag att cga gtg atc gaa gac atc gcc ggt cag 1075
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
 310 315 320 325
 ctg ggg cct ttt aac gtc cct gag aat ttc atc cca cag atc gac aaa 1123
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
 330 335 340
 aat ctg aaa gag ctg ttc gag agc taaacactga tgcacaagag cct 1170
 Asn Leu Lys Glu Leu Phe Glu Ser
 345

<210> 70

<211> 349

<212> BRT

<213> Corynebacterium glutamicum

<100> 70

Met Leu Asp Asn Ser Phe Tyr Thr Ala Gln Val Gln Gly Pro Tyr Glu
 1 5 10 15
 Thr Ala Ser Ile Gly Arg Leu Glu Leu Gln Gln Gly Gly Val Ile Glu
 20 25 30
 Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
 35 40 45
 Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
 50 55 60
 Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
 65 70 75 80
 Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
 85 90 95
 Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
 100 105 110
 Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
 115 120 125
 Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
 130 135 140
 Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
 145 150 155 160
 Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
195 200 205

Arg Glu Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
210 215 220

Lys Glu Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His
260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu
305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
340 345

4110-71

4111-1264

4112-DNA

4113-Corynebacterium glutamicum

4120-

4121-CD3

4122-1017...(1231)

4123-FXN00403

4400-71

tttttcagac tctgtgagaat gcaaaactaga cttagacagag ctgttcatat acaactggacg 60

aagtttttagt ctgttcacac cagaacaggc gggttatttc atg acc acc ctc ggg 115
Met Pro Thr Leu Ala
1 5

cct tca ggt caa ctt gaa atc caa ggg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

ggc gga gga atc att aca aac gct gaa atc gcc tat caa cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu

40	45	50	
cac gcc ctg act gga gat tcc aac gca gcc gat tgg tga gct gac ttg His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu 55 60 65			307
ctg ggt ccc gcc aac gcc atc aac act gat act ttc tgc gtg atc tgt Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys 70 75 80 85			355
acc aac gtc atc ggt ggt tga aac ggt tcc acc gga cct ggc tcc atg Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met 90 95 100			403
cat cca gat gga aat ttc tgg ggt aac ggc ttc ccc gcc acg tcc att His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile 105 110 115			451
cgt gat cag gta aac gcc gta aac cca ttc ctg gac gcc ctg ggc atc Arg Asp Gln Val Asn Ala Gln Lys Gln Phe Leu Asp Ala Leu Gly Ile 120 125 130			499
acc acc gtc gcc gca gta ctt ggt ggt tcc atg gat ggt gcc ggt acc Thr Thr Val Ala Ala Val Ser Gly Gly Ser Met Gly Gly Ala Arg Thr 135 140 145			547
ctg gag tgg gct gca atg ttc cca gaa act gtt gac gcc gct gtt gtc Leu Gln Trp Ala Ala Met Tyr Pro Gln Thr Val Gly Ala Ala Ala Val 150 155 160 165			595
ctt gcc gtt tct gcc cgc ggt acc gcc tgg cca atc ggt att cca tcc Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Leu Gly Ile Gln Ser 170 175 180			643
gcc cca att aag gag att gaa aac gac cag cag tgg cca gaa ggc aac Ala Gln Ile Lys Ala Ile Gln Asn Asp His His Trp His Gln Gly Asn 185 190 195			691
tac tac gaa tcc gcc tgc aac cca gcc acc gga ctg ggt gcc gcc gga Tyr Tyr Gln Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg 200 205 210			739
cgc atc gcc cag ctg acc tcc cgt ggt gaa ctg gaa atc gac gaa cgc Arg Ile Ala His Leu Thr Tyr Arg Gly Gln Leu Gln Ile Asp Gln Arg 215 220 225			787
ttc ggt acc aac gcc cca aag aac gaa aac cca ctg ggt ccc tac cgc Phe Gly Thr Lys Ala Gln Lys Asn Gln Asn Pro Leu Gly Pro Tyr Arg 230 235 240 245			835
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac tgg gac tac cca gca Lys Pro Asp Gln Arg Phe Ala Val Gln Ser Tyr Leu Asp Tyr Gln Ala 250 255 260			883
gac aag ctg gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctg acc Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr 265 270 275			931
gac gcc ctg aac cgc cac gac att ggt cgc gac cgc gga ggc ctg aac Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn 280 285 290			979

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc aac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat ggt ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tgg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Gln Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag 1254
 Gln Phe Tyr Ile
 375

<.10> 72

<.11> 177

<.12> PRT

<.13> Corynebacterium glutamicum

<.100> 72

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Gln Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Gln Lys Gln Phe Leu
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Gln Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Gln Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Gln Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

0010: 73

0011: 1210

0012: DNA

0013: Corynebacterium glutamicum

0200:

0201: CDS

0202: (101)..(1210)

0203: FFXA00463

0400: 73

tttttcagac tctgtgagaat gcaaaactaga cttagacagag ctgtccatat acactggacg 60

aagtttttagt cttgttcacc cagaacagge gggttttttc atg ccc acc ctc gcc 115
 Met Pro Thr Leu Ala
 1 5

ccg tca ggt caa ctt gaa atc caa ggc atc ggt gat gtc tcc acc gaa	163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	
10 15 20	
gac gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gga gat aaa gaa gga cgc agc aat gtc gtc ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ttc aat gga gat tcc aac gca gcc gat cgg cgg gct gat ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac aat gat att tac tgc gtg atc tgc	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80	
acc aac gtc atc ggt ggt ttc aac ggt tcc aac gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
85 90 95 100	
cac cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc aag tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cac gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc aag gtc gcc gca gta ctt ggt ggt tcc atc ggt ggt gcc cga acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gct gca atg tac cca gaa act gtc gcc gca gct gct gtc	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tat gca cgc gcc agc gcc tgg caa atc gcc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcc att gaa aac gac cac caa tgg cac gaa ggt aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc aac gga ctc gcc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc aac tac cgt ggt gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc gcc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883

Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260
 gac aag cta gta bag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275
 gac gcc ctc aac cgc cac gac att ggt gcc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290
 aag gcc ctc gaa tcc atc aaa gtt cca gtc att gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305
 acc gat att ttg tac ccc tac cac bag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325
 atg cga aat cta atg gcc atg gca aaa atc cta tcc cct gtc gcc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340
 gat cct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtc agg aac 1171
 Asp Ala Phe Leu Thr Gln Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355
 ttc tta agc ctc atc tcc cca gac aaa gac tcc cct acc 1210
 Phe Phe Ser Leu Ile Ser Pro Asp Gln Asp Asn Pro Ser
 360 365 370

X.10> 74

X.11> 170

X.12> PRT

X.13> *Corynebacterium glutamicum*

X.10> 74

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Asp Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser
 370

<110> 75
 <111> 687
 <112> DNA
 <113> Corynebacterium glutamicum

<120>
 <121> IDS
 <122> (101)..(664)
 <123> EXS03158

<400> 75

caaagctcacc cgaaggcacc aacggccaagt tgggtgttga caacaccttg gaatccccat 60
 acctgcagca gccactaaaa ctgggcgcac aegcaagtc ttg cac tcc acc acc 115
 Leu His Ser Thr Thr
 1 5
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20
 atc gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35
 gaa cgc atc cca tca gtt ttc gat gaa tac ctg acc gac cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50
 aag acc ctt gaa gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65
 atc ggc gaa ttc ctg gac tcc cgc cca gag gtc ttc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80 85
 cca ggt ctg aag aac cac cca ggc cac gaa gtc gaa ggc aag cag atg 403
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Glu Met
 85 90 95 100
 aag ggc ttc ggc ggc atg atc tcc gtc cgt ttc gaa ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115
 gaa gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Phe Ser Thr Lys Leu Ile Cys Leu Ala Glu
 120 125 130
 ttc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145
 cac cag tca ggt gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
 His Glu Ser Ala Ala Gly Ser Glu Leu Glu Val Pro Arg Asp Leu Val
 150 155 160 165
 ctc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
 170 175 180
 gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Glu Ala Leu Asn Asn Leu
 185

<110> 76

<111> 128

<112> PRT

<213> Corynebacterium glutamicum

<400> 76

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly
 1 5 10 15
 Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
 20 25 30
 Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
 35 40 45
 Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60
 Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
 65 70 75 80
 Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95
 Ala Ala Lys Glu Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110
 Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125
 Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140
 Pro Ala Thr Met Thr His Glu Ser Ala Ala Gly Ser Gln Leu Glu Val
 145 150 155 160
 Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
 165 170 175
 Ser Leu Ala Asp Val Gly Gln Ala Leu Asn Asn Leu
 180 185

1101 77
 1111 117
 1121 DNA
 1131 Corynebacterium glutamicum

1141
 1151 CDS
 1161 (1) (124)
 1171 FRXA00054

1181 77
 agc gca cta aaa ctc ggt gca cac gca gtc ttg cac tcc acc acc aag 48
 Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15
 tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96
 Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30
 gac cag gaa ctg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
 35 40 45
 cag atc gca tca gtt ttc gat gca tac ctg acc gcc cgt gcc ctc aag 192

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60
 acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80
 gag gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95
 ggt ctg aag aac cac cca ggc cac gaa gtc gca gag aag cag atg aag 336
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110
 cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384
 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125
 gct aag aag ttc tgt acc tcc acc aac ctg atc tgt ctg gcc gag tcc 432
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140
 ttc ggt ggc ctg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480
 Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145 150 155 160
 sag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gag ctc gtg ccc 528
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
 165 170 175
 ttc tcc att ggt att gaa gac att gaa gag ctg ctc gca gat gtc gag 576
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Gln
 180 185 190
 sag gcc ctc act aac ctt tagaaataa ttgaggcaca gca 617
 Gln Ala Leu Asn Asn Leu
 195

G10: 78

G11: 193

G12: PRT

G13: *Corynebacterium glutamicum*

G10: 78

Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
 35 40 45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145 150 155 160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
 165 170 175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
 180 185 190

Gln Ala Leu Asn Asn Leu
 195

<210> CDS

<211> (117)

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) (1147)

<223> EXA (153)

<400> CDS

gatgaatttt taacccaccat ctgtacccat taacccctggc tggcgtccac ccacagtaac 60

tgtgcaagcc ggaaggccag ccaggaactcc tggctggccgc atg aac cca cct atc 115
 Met Asn Pro Pro Ile
 1 5

acc ttc tcc acc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163
 Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
 10 15 20

gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta 211
 Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
 25 30 35

gat ggt ggg ttc gcc gta tct tat tct tca ggt ttg gca ggc gca aag 259
 Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
 40 45 50

tgg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa 307
 Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys
 55 60 65

gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc 355
 Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg
 70 75 80 85

gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val 90 95 100	403
att gct gct ggt caa ggt gca gat gtg ggg tgg gtg gaa tgg atc gct Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala 105 110 115	401
aat cgg aag atg gtg gta gct gat acc cct gca ata gtc gac ggt gtg Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val 120 125 130	409
cgt ggg cct gga gtt tgg act gtc gct gac ggg act ttc gca aag cca Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro 135 140 145	547
ctt cgt caa cgt caa ttp gaa ctt ggt gct gat act gtg ctt taa tgg Leu Arg Gln Arg Pro Leu Gln Leu Gly Ala Asp Ile Val Leu Tyr Ser 150 155 160 165	545
gca acc aaa ctt atc ggt gga caa cct gat ctt cct ctt gga gtc gca Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala 170 175 180	643
ctt cgt aag cct aag caa cat gca cag ctt ctt ggc act caa cct gat Val Cys Lys Ser Gln His His Ala Gln Phe Leu Ala Thr His Arg His 185 190 195	641
gat cat ggt caa atg aag gga ggt ctt gaa ggg ctt ctt gat cta cgt Asp His Gly Ser Val Pro Gly Gly Leu Gln Ala Phe Leu Ala Leu Arg 200 205 210	749
gga tgg cat tgg tgg gca gga cgt ctt gat cga gca gaa tgg aac gca Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala 215 220 225	747
gca gaa ctt tgg cgg cga ctt aac ggg cat ctt tgg gtt acc cgg gtc Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val 230 235 240 245	845
aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg 250 255 260	843
gtc cta ccc ttc gga tct gga aac atg tgg caa ttt gag ctt gat gca Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala 265 270 275	941
aca cct gaa cga act gat gaa att ctc gaa agc ctg caa ctt tta acc Thr Pro Gln Arg Thr Asp Gln Ile Leu Glu Ser Leu Ser Leu Leu Thr 280 285 290	979
cac ggg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr 295 300 305	1027
agg cgg gat gct gaa gtg gtc gca gaa gta ccg atg act ctt tgc cgc Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg 310 315 320 325	1075

ggt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac 1123
 Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn
 330 335 340

gac tca atc gac aaa gtt cta ggt tagaactcgt agccagtaac cag 1170
 Ala Ser Ile Asp Lys Val Leu Gly
 345

02100: 80

02110: 349

02120: PRT

02130: *Corynebacterium glutamicum*

04000: 80

Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu
 1 10 15

Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala
 20 25 30

Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly
 35 40 45

Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
 50 55 60

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
 65 70 75 80

Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
 85 90 95

Asn Thr Glu Glu Val Ile Ala Ala Ala Glu Gly Ala Asp Val Val Trp
 100 105 110

Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
 115 120 125

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
 130 135 140

Thr Phe Ala Thr Pro Leu Arg Glu Arg Pro Leu Glu Leu Gly Ala Asp
 145 150 155 160

Phe Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
 165 170 175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Glu Phe Leu
 180 185 190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
 195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
 210 215 220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
 225 230 235 240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His

245	250	255
Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser		
260	265	270
Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser		
275	280	285
Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala		
290	295	300
Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro		
305	310	315
Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu		
325	330	335
Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly		
340	345	

<310>=31

<311>=361

<312>=DNA

<313>=Corynebacterium glutamicum

<314>=

<315>=CDS

<316>=(131)..(338)

<317>=EX303159

<318>=31

```

aggggttagt tttaacacaaa agnaggacaga ttggtttatc atggacagaa gacagggttat 60
tttagggaca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
                                Leu Ser Phe Asp Pro
                                :
aac acc gag ggt ttc tcc act gca tcc att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
                                10                                15                                20
gac gac tac tac ggt tcc att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
                                25                                30                                35
ttc ggg gag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
                                40                                45                                50
cgt gtc ggc aac ccc acc atc gtc gca tta gag cac acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Glu Thr Val Ala Ala
                                55                                60                                65
ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
                                70                                75                                80
acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                                90                                95                                100

```

ctg ggc aac gat get tac ggc gga acc tac cgc ctg atc gac acc gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115
 ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
 Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
 120 125 130
 gaa gag gtc aag gca ggc atc aag gac aac acc aag ctg atc tgg gtg 547
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
 135 140 145
 gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
 Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
 150 155 160 165
 gca aac ctg acc gaa ggc acc aac ggc aac tgg gtt gtt gac aac acc 643
 Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
 170 175 180
 ttg cca tcc cca tac ctg cag cag cca cta aaa ctg ggc gca cca gca 691
 Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
 185 190 195
 aat ser tgc acc cca cca cca aat aca tgg aag gac act ccc acc ctg 739
 Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu
 200 205 210
 ttg acc gac ttg tgg gta cca aag acc agg aag tgg acc aag aac tgc 787
 Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys
 215 220 225
 tct tca tgc agg ggc gca tgg gac cga tcc cat cag ttt tgg atg cat 835
 Lys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His
 230 235 240 245
 acc tgaaccacccg ttggctccaaag acc 861
 Thr

c210 - f2

c211 - f46

c212 - PRP

c213 - *Corynebacterium glutamicum*

c400 - f2

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
 1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
 20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser

65	70	75	80
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro	85	90	95
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg	100	105	110
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val	115	120	125
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr	130	135	140
Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr	145	150	155
Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu	165	170	175
Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys	180	185	190
Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys	195	200	205
Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys	210	215	220
Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His	225	230	235
Ser Phe Ser Met His Thr	240	245	

62100- 42
 62110- 10-
 62112- DNA
 62113- Corynebacterium glutamicum

62114-
 62115- GDF
 62120- (1-1)..(701)
 62121- FEMAC2761

62119-
 62111- misc_feature
 62220- 59-,676,687,690,691,693
 62230- n = a, c, t, or g

62200-
 62210- VARIANT
 62220- 13.
 62230- Xaa = His or Gln

62200-
 62210- VARIANT
 62220- 19c
 62230- Xaa = Ile, Thr, Asn, or Ser

0220 -

0221 - VARIANT

0222 - 197

0223 - Kaa = Phe, Leu, Ser, Tyr, STOP CODON, Cys, or Trp

0220 -

0221 - VARIANT

0222 - 196

0223 - Kaa = Val, Ala, Glu, or Gly

0400 - 43

aggggtagt tttacacaaa agtggacagc ttgggtctatc attgcagaaa gacccggtcct 60

tttagggcca tagaattctg attacaggag ttgatctacc tgg tct ttt gac cca 115
Leu Ser Phe Asp Pro
1 3

ttt tcc cag ggt ttc tcc act gca tog att cac ggt ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
10 13 20

gat tac tac tac ggt tog att aac acc cca atc tat gac tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
23 30 33

ttt tcc cag aac ggt cca aac gaa ctg cgc aaa ggc tac gag tac acc 239
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
10 13 37

ttt tcc gga aac ccc acc atc gtg gca tta gag cag acc gtc gaa gaa 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
37 60 63

ttt gaa ggc gaa aag cat ggc cgc gaa ttt tcc tcc ggc atg gat gaa 335
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
37 73 80 83

acc gaa atc ctg ttc cgc atc atc ctc aag ccc ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
90 93 100

ttt ggc aac gat ggt tac ggc gga acc tac cgc ctg atc gac acc gta 461
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
103 110 113

ttt acc gaa tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtc 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
120 123 130

gaa gat gtc aag gaa ggc atc aag gac aac acc aag ggt gat ctt ggt 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
133 140 143

gaa aac ccc aac caa ccc agc act ttg gaa tta ccc gac atc gaa gaa 595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
150 153 160 163

gtt tgc aaa act tca ccc gaa agy cac caa ccc caa ggt tgt tgt ttg 643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
170 173 180

aca aca cct tgg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
 135 190 195

ang cac aag cag 703
 Xaa His Thr Gln
 200

<210> 24
 <211> 101
 <212> PPT
 <213> Corynebacterium glutamicum

<220>
 <221> VARIANT
 <222> 191
 <223> Xaa = His or Gln

<240>
 <241> VARIANT
 <242> 196
 <243> Xaa = Ile, Thr, Asn, or Ser

<260>
 <261> VARIANT
 <262> 197
 <263> Xaa = Phe, Leu, Ser, Tyr, STOP CODON, Cys, or Trp

<280>
 <281> VARIANT
 <282> 198
 <283> Xaa = Val, Ala, Glu, or Gly

<310> 24
 Val Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
 1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
 20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140

Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
145 153 158 160

Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
165 170 175

Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa
180 185 190

Pro Leu Lys Xaa Xaa Xaa His Thr Gln
195 200

110-85

111-111

112-DNA

113-Corynebacterium glutamicum

120-

121-CD3

122-121111(1091)

123-EXA (216)

140-85

ttgtgtatcag cgggcaaggca ggaagtgatc aactgctcag cggggatggg gacatcgtc 60

ttggtatcag cagcatctgc cagcagggaat cttatgaaaa ttg ggc gct tat ggt 115
Leu Gly Ala Tyr Gly
1

ttc ggt ggc att cat gga aaa tcc ggc ggc gaa ggc ggc gac att att 163
Leu Gly Ala Leu Pro Gly Lys Ser Ala Ala Gln Ala Ala Asp Ile Ile
10 15 20

cag ggt ggc aag ggc gat ctt ctc cat att cat cag ctt cgg ggc cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
25 30 35

ggt ttg cgt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Phe Val Gly Leu Leu Asp Met
40 45 50

ttc aac gtt gat cgc ggg ggc cga tct tgg gtc atg agc aca cgc ccc 307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
55 60 65

agg aga ttg aag ccc ctg acc ggc gat ttc ctt gac atg gat ttg gat 355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
70 75 80 85

ggg tgc gag gaa acc tgg gga acc ggc gtc gac aag cta aaa atc caa 403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
90 95 100

ttt gct ggt ccc tgg aat tta ggt ggc cgc att gag ttg ggc aat ggc 451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
105 110 115

cat cgc gtt ttg tct gat cgc ggt ggc atg cgt gat ctg acc cag ggc 499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala

120	125	130	
ctg atc gag ggc atc gat ggg cat gca cgc aag gtt gct ggg cga ttt			547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe			
135	140	145	
ggc gcc gaa gtg cag gtg caa att gat gag cgg gag ctg aaa tog ctt			595
Arg Ala Glu Val Glu Val Glu Ile Asp Glu Pro Glu Leu Lys Ser Leu			
150	155	160	165
atc gac ggc tcc ctg cct ggc act tcc acc ttt gac att att cct gag			643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala			
170	175	180	
gtg aat gtc gat gat gcc agt gaa cgt ttg cag cag gtc ttt agc tog			691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Glu Glu Val Phe Ser Ser			
185	190	195	
ttc cag ggg cgg aca tat ctg aac ctg acc ggc cag att cct act tgg			739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Glu Ile Pro Thr Trp			
200	205	210	
gat ctg ggt cgg ggt gcc ggc gcc gat act ggg cag att tcc atg gat			787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Glu Ile Ser Met Asp			
215	220	225	
caa ctg cgt gga aat gaa cat ttg gat ggt ttc ggt gaa acc atc aac			835
Ile Val Arg Gly Asn Glu Glu Leu Asp Gly Phe Gly Glu Thr Ile Thr			
230	235	240	245
agt cga atc cgg ctt ggt ttg ggc att acg aca gga aaa gat gtc gtc			883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val			
250	255	260	
gat caa cag ctg gag cga ccg cgg caa aag gcc gtt gag gta gca cgc			931
Asp Glu Leu Leu Glu Arg Pro Arg Glu Lys Ala Val Glu Val Ala Arg			
265	270	275	
ttc ttc gat cgt tta ggt gtg ggc cga aac tat ctg gtg gat gct gtc			979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val			
280	285	290	
gat att ctt cgg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc			1027
Asp Ile His Pro Gly Glu Asp Leu Val Glu Gly Thr Ile Thr Glu Ala			
295	300	305	
gag cag gat tat cgc atg gcc cgg gtg atg ttg gag atg ttg tog aag			1075
Ala Glu Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys			
310	315	320	325
gat tca tgc gac ctt taaggcttta ccggcgctgg gtg			1113
Asp Ser Cys Asp Leu			
330			

1210 - 86

1211 - 330

1212 - PBT

1213 - *Corynebacterium glutamicum*

1400 > 86

Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1 5 10 15
 Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
 20 25 30
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
 85 90 95
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110
 Gln Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190
 Glu Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205
 Glu Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220
 Glu Ile Ser Met Asp Glu Val Arg Gly Asn Glu His Leu Asp Gly Phe
 225 230 235 240
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
 245 250 255
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
 260 265 270
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
 275 280 285
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
 290 295 300
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
 305 310 315 320
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu

325

330

0210 - 87
 0211 - 551
 0212 - DNA
 0213 - Corynebacterium glutamicum

0220 -
 0221 - CDS
 0222 - (1)...(528)
 0223 - EXA02187

0210 - 87
 gag gaa cgg atg cgc ttt aac ttc cca cgg cag cag cgg ggc agg ttc 48
 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
 1 5 10 15

tgg tgg atc gag gat ttc att cgg cca cgg gag caa gct gtc aag gac 96
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Gln Gln Ala Val Lys Asp
 20 25 30

agg gaa gtg gag gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144
 Gly Glu Val Asp Val Met Pro Phe Glu Leu Val Thr Met Gly Asn Pro
 35 40 45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

tat ttg gaa gtt cac ggc atc ggg gtg cag ctg acc gaa gca tgg gcc 240
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

gag tac tgg cac tcc cga gtg cgg agc gaa ctg aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

agg tct gtc ggt gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

tta gat tac agc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctg gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

atc ggc gtg gag ttg tcc gag gaa ctg cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

aca gac ggc ttt gtg ctg tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

taacaccttt gagagggaaa act 551

0210 - 83
 0211 - 176
 0212 - PRT
 0213 - *Corynebacterium glutamicum*

0400 - 83
 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
 1 5 10 15
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 Hu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

0210 - 83
 0211 - 176
 0212 - DNA
 0213 - *Corynebacterium glutamicum*

0400 -
 0401 - CDS
 0402 - (101)..(2599)
 0403 - EXON2198

0400 - 83
 agactagtggtt cgttttgctt gtgttgotta ggcggcgttg aaaatgaact acgaatgaaa 60
 agttcggggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5
 act tca tca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc	311
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu	
25 30 35	
caa ggc ttt gac ctg gac gtc gaa aag gat ttc ctt gat ctg gag ggg	359
Gln Gly Phe Asp Leu Asp Val Gln Lys Asp Phe Leu Asp Leu Glu Gly	
40 45 50	
cgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att	407
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile	
55 60 65	
cac cgc gcc tac ttt gag ggc gga gct gac ttg gtt gag acc aat act	455
His Arg Ala Tyr Phe Gln Ala Gly Ala Asp Leu Val Gln Thr Asn Thr	
70 75 80 85	
ttt ggt tgc aac ctg cgg aac ttc ggc gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
cgc cgt gac ctt gcc tac aag cgt act gca gtg ctt agg gaa ttg gct	451
Cys Arg Gln Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Gln Val Ala	
110 115 120	
gat gag atg ggc cgc gcc cca aat ggc atg cgg cgt ttc gtg att ggt	499
Asp Gln Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
125 130 135	
acc ctg gga cct gga aag aag ctt cca tcc ctg cgc act gca cag cat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
gla gat ttg cgt agg cca tac aac gaa gca ggc ctt ggc atc atc gac	595
Ala Asp Leu Arg Gly His Tyr Lys Gln Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
ggt ggt gcc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Gln Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct ggc ctt cac gcc gtt cca gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Gln Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cag gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg ggt tct gag atc tgt gcc ggc ttg aca ggc ctg cag cca	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
tgc gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931

Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala	
			265					270					275			
gaa	tac	cca	ctt	gag	gct	gag	gat	ttg	gag	cag	gag	ctg	gct	gga	ttc	979
Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe	
		280					285					290				
gtc	tcc	aaa	tat	ggc	ctg	tcc	atg	gtg	ggt	ggt	tgt	tgt	ggc	acc	aca	1027
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr	
	295					300					305					
cct	gag	aac	atc	ggt	ggc	gtc	ggc	gat	ggc	gtg	gtt	ggt	gtt	cca	gag	1075
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu	
310					315					320					325	
cag	gaa	acc	tcc	aca	ctg	aac	cag	atc	cct	cca	ggt	cct	gtt	gac	cag	1123
Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	Gly	Pro	Val	Gln	Gln	
				330					335					340		
gac	tcc	agg	gag	gtc	gag	aaa	cag	gac	tcc	gtc	ggt	tcc	ctg	tac	acc	1171
Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	Ala	Ser	Leu	Tyr	Thr	
		345					350						355			
tcc	gtg	cca	tig	tcc	cag	gaa	acc	ggc	att	tcc	atg	atc	ggt	gac	ggc	1219
Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser	Met	Ile	Gly	Gln	Arg	
		360					365					370				
acc	aac	tcc	aac	ggt	tcc	agg	cca	tcc	ggt	cag	cca	atg	ctg	tcc	ggc	1267
Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	Ala	Met	Leu	Ser	Gly	
	375					380						385				
gat	tgg	aaa	atg	tgt	gtg	gat	cct	gaa	agg	cag	caa	acc	ggc	gat	ggt	1315
Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	Gln	Thr	Arg	Asp	Gly	
390					395					400				405		
gca	aac	atg	ctg	act	cct	tct	atg	gat	tac	ctg	gga	aga	gac	ggt	acc	1363
Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val	Gly	Arg	Asp	Gly	Thr	
			410					415						420		
gac	gat	atg	ggc	acc	ctg	gaa	aaa	cct	ctt	gct	acc	agg	tcc	act	ctg	1411
Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala	Thr	Ser	Ser	Thr	Leu	
			425					430					435			
cca	atc	atg	att	gac	tcc	acc	cag	cca	gag	gtt	att	ccc	aca	ggt	ctt	1459
Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val	Ile	Arg	Thr	Gly	Leu	
		440					445					450				
gag	aac	tig	ggt	gga	aga	agg	atc	gtt	aac	tcc	gtc	aac	ttt	gac	gac	1507
Glu	His	Leu	Gly	Gly	Arg	Ser	Ile	Val	Asn	Ser	Val	Asn	Phe	Glu	Asp	
		455				460					465					
ggc	gat	ggc	cct	gag	tcc	aga	tac	cag	ggc	atc	atg	aaa	ctg	gtc	aac	1555
Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile	Met	Lys	Leu	Val	Lys	
470					475					480				485		
cag	aac	ggt	ggc	gac	gtg	gtt	ggc	ctg	acc	att	gat	gag	gaa	ggt	cag	1603
Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile	Asp	Glu	Glu	Gly	Gln	
			490					495						500		
gca	ggt	acc	ggt	gag	caa	agg	gtg	ggc	att	gct	aaa	aga	ctg	att	gac	1651
Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala	Lys	Arg	Leu	Ile	Asp	

505	510	515	
gat atc acc ggt agc tac ggc ctg gat atc aaa gac atc gtt gtg gac Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp 520 525 530			1699
tac ctg acc ttc cgg atc tct act ggc cag gaa gaa acc agg cga gat Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Gln Thr Arg Arg Asp 535 540 545			1747
ggc att gaa acc atc gaa gcc atc cgc gag cag aag aag ctg tac cca Gly Ile Glu Thr Ile Glu Ala Ile Arg Gln Leu Lys Lys Leu Tyr Pro 550 555 560 565			1795
gaa atc cgc acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac Gln Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn 570 575 580			1843
ctt gct gaa cgt cag gtt ctt aac tct gtg ttc ctc aat gaa tgc att Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile 585 590 595			1891
gag gct ggt ctg gac tct ggc att gag cag aac tcc aac att ttc cgg Gln Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro 600 605 610			1939
atg aac cgc att gat tat cgc cag cgc gaa gty ggc ttc gat atg gtc Met Asn Arg Ile Asp Asp Arg Gln Arg Gln Val Ala Leu Asp Met Val 615 620 625			1987
ctt gat cgc cgt acc gag gat tac gat cgg ctg cag gaa ttc atg aag Tyr Asp Arg Arg Thr Gln Asp Tyr Asp Pro Leu Gln Gln Phe Met Gln 630 635 640 645			2035
agg ttc cag ggt gtt tct gct gcc gat gcc aag gat gct cgc gct gaa Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Gln 650 655 660			2083
cag ctg cgc gct atg cct ctg ttc gag cgt ttc gca cag cgc atc atc Gln Leu Ala Ala Met Pro Leu Phe Gln Arg Leu Ala Gln Arg Ile Ile 665 670 675			2131
gac ggc gat aac aat ggc ctt gag gat gat ctg gaa gca gcc atg aag Asp Gly Asp Lys Asn Gly Leu Gln Asp Asp Leu Glu Ala Gly Met Lys 680 685 690			2179
gag aag tct cct att ggc atc atc aac gag gac ctt ctg aac ggc atg Gln Lys Ser Pro Ile Ala Ile Ile Asn Gln Asp Leu Leu Asn Gly Met 695 700 705			2227
aag acc gtg ggt gag ctg tct ggt tcc gga cag atg cag ctg cca ttc Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe 710 715 720 725			2275
gtg ctg caa tct gca gaa acc atg aaa act ggc gtg gcc tat ttc gaa Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu 730 735 740			2323
cgg ttc atg gaa gag gaa gca gaa gct acc gga tct ggc cag gca gag Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu 745 750 755			2371

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467
 Ile Gly Lys Asn Leu Val Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

ggc gaa gaa cac aac gaa gac gtc atc ggc atg tgg gga ctt ctt gtg 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc acc gtg gtc atg aag caa acc atc agc gac 2599
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
 825 830

<310> 90

<311> 823

<312> PRT

<313> Corynebacterium glutamicum

<400> 90

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
 20 30

Met Gly Thr Glu Leu Glu Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Glu Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95

Asp Ile Ala Asp Arg Cys Arg Ser Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Glu Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Glu Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Glu
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala

500					505					510					
Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys
515					520					525					
Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu
530					535					540					
Glu	Thr	Arg	Arg	Asp	Gly	Ile	Gln	Thr	Ile	Glu	Ala	Ile	Arg	Gln	Leu
545					550					555					
Lys	Lys	Leu	Tyr	Pro	Gln	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile
565					570					575					
Ser	Phe	Gly	Leu	Asn	Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe
585					590					595					
Leu	Asn	Gln	Cys	Ile	Gln	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser
605					610					615					
Ser	Lys	Ile	Leu	Pro	Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Gln	Val
620					625					630					
Ala	Leu	Asp	Met	Val	Tyr	Asp	Arg	Arg	Thr	Gln	Asp	Tyr	Asp	Pro	Leu
635					640					645					
Gln	Gln	Phe	Met	Gln	Leu	Phe	Gln	Gly	Val	Thr	Ala	Ala	Asp	Ala	Lys
655					660					665					
Asp	Ala	Arg	Ala	Gln	Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Gln	Arg	Leu
670					675					680					
Ala	Gln	Arg	Ile	Ile	Asp	Gly	Asp	Lys	Asn	Gly	Leu	Gln	Asp	Asp	Leu
685					690					695					
Gln	Ala	Gly	Met	Lys	Gln	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Gln	Asp
700					705					710					
Leu	Leu	Asn	Gly	Met	Lys	Thr	Val	Gly	Gln	Leu	Phe	Gly	Ser	Gly	Gln
715					720					725					
Met	Gln	Leu	Pro	Phe	Val	Leu	Gln	Ser	Ala	Gln	Thr	Met	Lys	Thr	Ala
730					735					740					
Val	Ala	Tyr	Leu	Gln	Pro	Phe	Met	Gln	Gln	Gln	Ala	Gln	Ala	Thr	Gly
745					750					755					
Ser	Ala	Gln	Ala	Gln	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys
760					765					770					
Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser
775					780					785					
Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser
790					795					800					
Ala	Met	Leu	Gln	Ala	Ala	Gln	Gln	His	Lys	Ala	Asp	Val	Ile	Gly	Met
805					810					815					
Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	Val	Met	Lys	Gln	Thr	Ile	Ser
820					825					830					

Asp

<210> 91
 <211> 2578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (191)..(2578)
 <223> FRXA02196

<240> 91
 agactagtgg cggtttgact gtgttgatta ggoggcggtg aaaatgaact acgaatgaaa 60
 atttggggaa ttgtataatc cgtactaagc tgtatcacaa atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5
 act tca caa gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat ggg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg caa aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctg 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35
 caa gcc ttt gac ctg gac gtg gaa aag gat tcc ctg gat ctg gag ggg 259
 Ala Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50
 tct aat gag att ctg aac gac acc cgc cct gat gtg ttg agg cag att 307
 Lys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65
 caa gcc gcc tac ctg gag ggc gga gct gac cgg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85
 ttt ggt tgc aac ctg cgg aac ttg ggc gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100
 ttc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
 105 110 115
 gat gag atg ggg cgg ggc cca aac ggc atg cgg cgt ttc gtg gtt ggt 499
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
 120 125 130
 ttc ctg gga cct gga acg aag ctt caa tgg ctg ggc cat gca cgg tat 547
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
 135 140 145
 gaa gat ttg cgt ggg cac ttc aag gaa gca ggc ctt ggc atc atc gac 595
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
 150 155 160 165

ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct ggc gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att ttc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
210 205 210	
atg ctc atg ggt cct gag atc ggt gcc ggc ttg aca gcc ctg cag cca	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att gtt ctg aac tgc gcc acc ggt cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg acc gag cac ctg ggt ttc ctg tcc aag caa gcc gat att cct gtc	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
ccc gtc atc cct aac gca gtt ctt cct gtc ctg ggt aac aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tcc cca att gag gct gag gat ttg gcc cag gcc ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Gln Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
ctc tcc gaa tat gcc ctg tcc atg gtc ggt ggt tgt tgt gcc acc aca	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct cag cac atc cgt gcc gtc gcc gat gcc ctg gtc ggt gtt cca gag	1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	
cag gaa acc tcc aca ctg acc aag atc cct gca gcc cct gtt gag cag	1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
330 335 340	
gcc tcc cgt gag gtg gag aac gag gac tcc gtc gcc tcc ctg tcc acc	1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
345 350 355	
tcc gtc cca ttg tcc cag gaa acc gcc att tcc atg atc ggt gag cgc	1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
360 365 370	
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg cct gcc	1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
375 380 385	
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt	1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
390 395 400 405	

goa cac atg ctg gat ctt tgt gtg gat tac gtg gga cca gac ggc acc	1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
410 415 420	
gac gat atg gag acc tgg gaa gaa ctt ctt gct acc aac tcc acc tgg	1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	
425 430 435	
cca atc atg att gac tcc aac gag cca gag gtt att cgc acc ggc ctt	1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
440 445 450	
gac cac atg cgt gga cca aac atc gtt aac tcc gtc aac ttt gaa gac	1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
455 460 465	
ggc gat ggc cct gag tcc ccc tac cag cgc atc atg aaa ctg gta aag	1555
Gly Asp Gly Pro Glu Ser Arg Tyr Glu Arg Ile Met Lys Leu Val Lys	
47 475 480 485	
caa cac tgt gag gcc gtg gtt gag ctg acc att gat gag gaa gta cag	1603
Glu His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Glu	
490 495 500	
gca cgt acc gct gag cac aag gtc cgc att gct aac cca ctg att gac	1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
505 510 515	
gat atc acc ggc agc tac gac ctg gat atc aaa gac aac gtt gtc gac	1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
520 525 530	
tgc ctg acc ttc cag atc tct act ggc cag gaa gaa aac agg cca gat	1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Glu Glu Glu Thr Arg Arg Asp	
535 540 545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctg tac cca	1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro	
550 555 560 565	
gaa atc cac aac acc ctg gct ctg tcc aat att tcc ttc ggc ctg aac	1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
570 575 580	
cat gct gaa cgc cag gtt ctt aac tct gtg ttc ctg aat gag tgc att	1891
Pro Ala Ala Arg Glu Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile	
585 590 595	
gaa gct ggt ctg gac tct gag att gag cac agc tcc aag att tgg cag	1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	
600 605 610	
atg aac cgc att gat gat cgc cag cgc gaa gtg gag tgg gat atg gtc	1987
Met Asn Arg Ile Asp Asp Arg Glu Arg Glu Val Ala Leu Asp Met Val	
615 620 625	
tat gat cgc cgc acc gag gat tac gat cgc ctg cag gaa ttc atg cag	2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Glu Glu Phe Met Glu	
630 635 640 645	
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa	2083

Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys	Asp	Ala	Arg	Ala	Glu		
				650					655						660		
cag	ctg	gac	gct	atg	ccg	ttg	ttt	gag	cgt	tig	gca	cag	cgc	atc	atc		2131
Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu	Ala	Gln	Arg	Ile	Ile		
				665				670						675			
gac	gpc	gat	aag	aat	ggc	ott	gag	gat	gat	ctg	gaa	gca	ggc	atp	aag		2179
Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu	Glu	Ala	Gly	Met	Lys		
				680				685						690			
gag	aag	tct	ccg	att	ggc	atc	att	aac	gag	gac	ott	ctc	aac	ggc	atg		2227
Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp	Leu	Leu	Asn	Gly	Met		
				695			700							705			
aag	acc	gtg	ggt	gag	ctg	ttt	ggt	ccc	gga	cag	atg	cag	ctg	cca	ttc		2275
Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln	Met	Gln	Leu	Pro	Phe		
						715					720				725		
gtg	ctg	caa	tgg	gca	gaa	acc	atg	aaa	act	ggc	ctg	gca	tat	ttg	gaa		2323
Val	Leu	Gln	Ser	Ala	Glu	Thr	Met	Lys	Thr	Ala	Val	Ala	Tyr	Leu	Glu		
						730				735					740		
cag	ttc	atg	gaa	gac	gaa	gca	gaa	gct	acc	gga	tct	ggc	cag	gca	gag		2371
Pro	Phe	Met	Glu	Glu	Ala	Glu	Ala	Thr	Gly	Ser	Ala	Gln	Ala	Glu			
						745				750				755			
gtc	gag	ggc	aaa	atc	gtc	gtg	gca	acc	gtc	aag	ggt	gac	gtg	caa	gat		2419
Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys	Gly	Asp	Val	His	Asp		
							765							770			
atc	gpc	aag	aac	ttg	gtg	gac	atc	att	ttg	ccc	aac	aac	ggt	ccg	gac		2467
Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser	Asn	Asn	Gly	Tyr	Asp		
							780							785			
gtg	ctg	aac	ttg	ggc	atc	aag	cag	cca	ctg	ccc	ggc	atg	ttg	gaa	gca		2515
Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser	Ala	Met	Leu	Glu	Ala		
							795				800				805		
ggc	caa	gaa	cac	aaa	gca	gac	gtc	atc	ggc	atg	tgg	gga	ctt	ctt	gtg		2563
Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met	Ser	Gly	Leu	Leu	Val		
						810				815				820			
aag	ccc	acc	gtg	gtg													2578
Lys	Ser	Thr	Val	Val													

C110 - 92

C111 - 916

C112 - PBT

C113 - Corynebacterium glutamicum

C100 - 92

Met	Ser	Thr	Ser	Val	Thr	Ser	Pro	Ala	His	Asn	Asn	Ala	His	Ser	Ser		
1				5					10					15			

Glu	Phe	Leu	Asp	Ala	Leu	Ala	Asn	His	Val	Leu	Ile	Gly	Asp	Gly	Ala		
				20				25							30		

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe

35	40	45
Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp 50 55 60		
Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu 65 70 75 80		
Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr 85 90 95		
Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val 100 105 110		
Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg 115 120 125		
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu 130 135 140		
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala 145 150 155 160		
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala 165 170 175		
Gln Asp Leu Leu Gln Val Lys Ala Arg Val His Gly Val Gln Asp Ala 180 185 190		
Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val 195 200 205		
Gln Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu 210 215 220		
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala 225 230 235 240		
Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His 245 250 255		
Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu 260 265 270		
Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln 275 280 285		
Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly 290 295 300		
Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val 305 310 315 320		
Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala 325 330 335		
Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val 340 345 350		
Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser 355 360 365		

Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Pro Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
 725 730 735
 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
 740 745 750
 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
 755 760 765
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 770 775 780
 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
 785 790 795 800
 Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
 805 810 815
 Ser Gly Leu Leu Val Lys Ser Thr Val Val
 820 825

K10 - 93
 K11 - 621
 K12 - DNA
 K13 - *Corynebacterium glutamicum*

K20 -
 K21 - CDS
 K22 - (101)...(898)
 K23 - EXN03074

K4 0 - 93
 atgtggggga atctgggttt ttgtgaattg tgtgggatga atctctttaa aattcacatt 60
 tagcaggaga agcatactgt ttaagttcta tgcctggggc atg act caa agt got 115
 Met Thr Gln Ser Ala
 1 5
 caa gaa ttc att ggc acc gca gac ctg gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 got caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Gln
 25 30 35
 tct cag gga ata ata acc acc gtg aca tgc ttc caa gac aac gcc ctg 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac cgg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tgg att ggt ggc att cac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac ggc gac tct gac gga att atc gtc acc gac gcc cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 caa taatttgttt tgaagagcga gta 621
 Glu

<210> 64

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Thr Glu Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Glu Ser Cys Asp Thr Glu Phe Glu Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Glu Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
145 150 155 160

Glu Ala Pro Ile Lys Gln
165

K110- 95

K111- 621

K112- DNA

K113- *Torynebacterium glutamicum*

K120-

K121- CDS

K122- (101)...(598)

K123- FRXA12906

K100- 95

tttggtggca atctgggttt ttgttaattg tctgggatga atctcttaaa aattcacatt 60

ttgtgggaca agcataactgt tttagttcta tctgtggggt atc act caa agt gct 115
Met Thr Gln Ser Ala
1 5

caa caa ttc att gct acc gca gac ctg gta gac atc atc ggc gac aac 163
Pro Gln Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
11 15 20

ggc caa tca tgc gac act cag ttt caa aac ctg gga ggt gct aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Gln
25 30 35

tta caa gga ata ata acc acc gtg aaa tgc ttc caa gac aac ggc ctg 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
40 45 50

tta caa tcc atc ctg agc gag gat aat cct ggc gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Gln Asp Asn Pro Gly Gly Val Leu Val Ile
55 60 65

gat tgc gac gta tcc gtg caa acc ggc sta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
70 75 80 85

gga ctg gga aaa gat cat ggt tgg tcc gca gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Prp Ser Gly Val Ile Val Asn Gly Ala
90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
105 110 115

ctt tga acc aac cgg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
120 125 130

gac sta gtg gta tgg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
135 140 145

gtc tac ggc gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

gag taatttggtt tgaagagga gta 621
 Gln

42100: 26
 42110: 166
 42112: PET
 42116: Corynebacterium glutamicum

4400: 26
 Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15

12: Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

32: Gly Ala Thr Glu Pro His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

52: Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 55 60

62: Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

82: Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

102: Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

122: Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

142: Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

162: Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

182: Ala Pro Ile Lys Gln
 165

42100: 97
 42110: 1367
 42112: DNA
 42116: Corynebacterium glutamicum

42100:
 42110: SDS
 42112: (111) (1534)
 42116: EXN00132

14000: 97
 aasagettca atcaattogg tgtccattcc aacatgtaga gtggtgcgcg ttaaaaaagt 60

tttcttaatt ttcattttct taaaaggagc tcgpcaggac atg gca cag gtt atg	115
Met Ala Gln Val Met	
1 5	
gac ttc aag ggt gcc gat ctt tca cta gca gag gca gga cgt cac cag	163
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln	
10 15 20	
att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttc cgc aag	211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys	
25 30 35	
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt cct	259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser	
40 45 50	
atc cac atg aag gtc cag acc ccc gtc ctt att gag acc ctc act gct	307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala	
55 60 65	
cag gcc act gag ggt cgt tgg gct tcc tgc aac att ttc ccc acc cag	355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln	
70 75 80 85	
gat gag act gca gcc ggt atc gtt gtc ggc tcc ggc acc gtc aac gag	403
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu	
90 95 100	
cca gct cgt ggt cca gta ttc cca tgg aag ggt gag tca ctg gag gag	451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu	
105 110 115	
cac tgg tgg tgg atc aac cag atc ttc agc tgg ggc gat gag ctg cca	499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro	
120 125 130	
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc	547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg	
135 140 145	
ggt cgc aac cac gag cag cgt ggt ctg gtt cca cca gca gag gcc aac	595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn	
150 155 160 165	
gat ccc gat gag tac atc gca ttc ctg ggc atg ctg cgt gag gtt ctc	643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu	
170 175 180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt	691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly	
185 190 195	
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct	739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala	
200 205 210	
gaa gaa ggc gtg ctg cct ttc cca ggc atg aac gtc aac gac gct gtc	787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val	
215 220 225	

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc	835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile	
233 235 241 243	
gac ggc atc aac cgc gcc aat gac atg ctg atg ggc ggc aag aac gtg	883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val	
253 255 258 260	
ctt gtc tgc ggt tac gcc gat gtc gcc aag cgc tgc gct gag gct ttc	931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	
265 270 275	
gac ggc cag ggt gat gcc gtc aag gtc acc aac gct gac cca atc aac	979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	
281 283 291	
gct ctt cag ggt ctg atg gat ggc tac tct ctg gtc acc att gat gag	1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	
295 300 305	
gcc atc gag gac gcc gac atc gtg atc acc cgc acc gcc aac aag gac	1075
Ala Ile Glu Asp Ala Asp Ile Val Leu Thr Ala Thr Gly Asn Lys Asp	
311 315 320 321	
atc att tcc ttc gag cca atg ctg aac atg aag gat cag gct ctg ctg	1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Cys Asp His Ala Leu Leu	
325 330 335 340	
gcc aac atc ggt cca ttt gat aat gag atc gat atg cat tcc ctg ctg	1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	
345 350 355	
ccc cgc gcc gcc gtc acc cgt acc aag atc aag ccc cag atc gag gag	1219
His Arg Asp Asp Val Thr Arg Thr Ile Lys Pro Gln Val Asp Glu	
361 365 371	
ttc acc ttc ttc acc ggt cgc tcc atc atc atc ctg tcc tcc gaa ggt cgc	1267
Phe Thr Phe Ser Phe Gly Arg Ser Leu Ile Val Leu Ser Glu Gly Arg	
375 380 385	
ctg ctg aac att gcc aac gcc acc gaa cag cca tca ttt gtc atg tcc	1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser	
390 395 400 405	
aac tct ttc gat gat cag acc att ggc cag atc gaa ctg ttc caa aac	1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn	
410 415 420	
gaa gga cag tcc gag aac gag gcc tac cgt ctg cct aag gtt ctg gac	1411
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp	
425 430 435	
gaa aag gtg gaa cgc atc cag gtt gag gct ttc gcc ggt cag ctg acc	1459
Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr	
440 445 450	
gaa ctg acc aag gag cag gct gag tac atc gcc gtt gac gtt gca gcc	1507
Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly	
455 460 465	
cca ttc aag cgc gag cag tac cgc tac taatgattgt cagcattgag gga	1557

Pro Phe Lys Pro Glu His Tyr Arg Tyr
470 475

0110 - 98

0111 - 473

0112 - PRT

0113 - Corynebacterium glutamicum

0400 - 98

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
1 5 10 15

Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser
85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
100 105 110 115

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
145 150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
165 170 175

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
180 185 190

Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
195 200 205

Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
210 215 220

Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
225 230 235 240

Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
245 250 255

Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
260 265 270

Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
 290 295 300
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys
 325 330 335
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
 340 345 350
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
 355 360 365
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro
 385 390 395 400
 Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
 405 410 415
 Glu Leu Phe Glu Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 420 425 430
 Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu
 435 440 445
 Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly
 450 455 460
 Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr
 465 470 475

4110-39

4111-12:

4112-DNA

4113-Corynebacterium glutamicum

4120-

4121-CDS

4122-(1...)(105)

4123-FRMA00132

4400-39

cat gtt gag ggt ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag 48
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15

ggt cag ttc atc ggc gtt gac gtt gca ggc cca ttc aag cag gag cac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

ttc agc ttc taatgattgt cagcattgag gga 128
 Tyr Arg Tyr

35

1210 - 100

1211 - 31

1212 - PRT

1213 - *Corynebacterium glutamicum*

1400 - 100

His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15

Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

Tyr Arg Tyr

35

1210 - 101

1211 - 1396

1212 - DNA

1213 - *Corynebacterium glutamicum*

1220 -

1221 - CDS

1222 - (101)..(1396)

1223 - FRXA01:71

1430 - 101

tacaatttc atcaattggg tgcacatcc aacatctaga gtagtgaggg ttaaaaaagt 60

tttcataat ttcatittct taaaaggagg tggcaggag atg gca cac gtt atg 115
 Met Ala Gln Val Met
 1 5

gac ttc aag gtt ggc gat ctt tca cta gca gag gca gga cgt cac bag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
 10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cga aag 211
 Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
 25 30 35

gaa ttc gca gag gag cag cct ttg aag ggc gcc cga att gct ggt tct 259
 Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
 40 45 50

atc cac aag aag gtc cag acc gcc gtc ctt att gag acc ctc act gct 307
 Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala
 55 60 65

ttg agc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc bag 355
 Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln
 70 75 80 85

gat gag gct gca gcc gct atc gtt gtc gcc tcc gcc acc gtc gaa gag 403
 Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu
 90 95 100

cca gct ggt gtt cca gta ttc gcc tgg aag ggt gag tca ctg gag gag 451

Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu		
			105						110								
tac	tgg	tgg	tac	ata	aac	cag	atc	ttc	agc	tgc	ggc	gat	gag	ctg	cca	499	
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro		
			120										130				
aac	atg	atc	ctc	gac	gac	ggc	ggt	gac	gac	acc	atg	gct	gtt	att	cgc	547	
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg		
			135										145				
ggc	cgc	gaa	tac	gag	cag	gct	ggt	cgc	gtt	cca	cca	gca	gag	gac	aac	595	
Gly	Arg	Gln	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn		
																160	
gat	tcc	gat	gac	tac	atc	gca	tcc	tgc	ggc	atg	ctg	cgt	gag	gtt	ctt	643	
Asp	Ser	Asp	Gln	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu		
																170	
gct	gca	gag	cat	ggc	aag	cgc	ggc	aag	atc	ctt	cag	gct	gtt	aag	ggt	691	
Ala	Ala	Gln	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Gln	Ala	Val	Lys	Gly		
																185	
gtc	atc	gag	gac	acc	atc	acc	ggt	gtg	cac	tgc	ctg	tac	cac	tcc	gct	739	
Val	Thr	Gln	Gln	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala		
																200	
gaa	gaa	ggc	gtg	ctg	cat	ctc	cac	ggc	ctg	cac	ctc	aac	gac	gct	gtt	787	
Gln	Gln	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val		
																215	
acc	aag	tcc	aag	ttt	gac	aac	aac	tac	ggc	acc	ggc	cac	tcc	ctg	atc	835	
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile		
																230	
gac	ggc	atc	aac	cgc	gct	act	gac	atg	ctc	ctg	ggc	ggc	aag	aac	gtg	883	
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val		
																250	
ctt	gtc	tgc	gtt	tac	ggc	gat	gtc	ggc	aag	ggc	tgc	gct	gag	gct	ttc	931	
Leu	Val	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys	Gly	Cys	Ala	Glu	Ala	Phe		
																265	
gac	ggc	cag	gac	gct	cgc	gtc	aac	gtc	acc	cac	gct	gac	cca	atc	aac	979	
Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Gln	Ala	Asp	Pro	Ile	Asn		
																280	
gct	ctt	cag	gct	ctg	atg	gat	ggc	tac	tct	ctg	ctc	acc	gtt	gat	gag	1027	
Ala	Leu	Gln	Ala	Leu	Met	Asp	Gly	Tyr	Ser	Val	Val	Thr	Val	Asp	Glu		
																295	
gac	atc	gag	gac	ggc	gac	atc	gtg	atc	acc	ccc	acc	ggc	aac	aag	gac	1075	
Ala	Ile	Glu	Asp	Ala	Asp	Ile	Val	Ile	Thr	Ala	Thr	Gly	Asn	Lys	Asp		
																310	
atc	att	tcc	ttc	gag	cag	atg	ctc	aag	atg	aag	cat	cac	gct	ctg	ctg	1123	
Ile	Ile	Ser	Phe	Glu	Gln	Met	Leu	Lys	Met	Lys	Asp	His	Ala	Leu	Leu		
																330	
ggc	aac	atc	ggt	cac	ttt	gat	aat	gag	atc	gat	atg	cat	tcc	ctg	tgc	1171	
Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp	Met	His	Ser	Leu	Leu		

345	350	355	
cac cgc gac gac gtc acc cgc acc aag atc ang cca cag gtc gac gag			1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu			
360	365	370	
ttc acc ttc ttc acc ggt cgc ttc atc atc gtc ctg ttc gaa ggt cgc			1267
Phe Thr Phe Ser Thr Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser			
375	380	385	
ctg ttg aac ctt ggc aac ggc acc gga cac cca tca ttt gtc atg ttc			1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser			
390	395	400	405
aac tct ttc ggc gat cag acc att ggc cag atc gaa ctg ttc cca aac			1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn			
410	415	420	
gaa cga cag taa gag aac gag gtc taa cgt ctg			1396
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu			
425	430		
<p><210> 102 <211> 432 <212> PRT <213> Corynebacterium glutamicum</p>			
<p><410> 102</p>			
Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu			
1	1	15	1
Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu			
20	25	30	
Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala			
35	40	45	
Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile			
50	55	60	
Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn			
65	70	75	80
Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser			
85	90	95	
Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly			
100	105	110	
Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp			
115	120	125	
Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr			
130	135	140	
Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro			
145	150	155	160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met			
165	170	175	

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
 260 265 270
 Lys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
 290 295 300
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Phe Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys
 325 330 335
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Gln Ile Asp
 340 345 350
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
 355 360 365
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro
 385 390 395 400
 Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
 405 410 415
 Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 420 425 430

<110> 101

<111> 2358

<112> DNA

<113> Corynebacterium glutamicum

<110>

<111> CDS

<112> (101)...(2335)

<113> RXN02085

<400> 103

caccocgggtga tttagogagaac attgaaaacat cgtcagaaga ttgocgtgog tccatagocgg 60
 gatccgcacag ttoggtctcaa gcagaaaagtc ttttaactcac atg act tcc aac ttt 115
 Met Thr Ser Asn Phe
 1 5
 tct tcc act gtc gct ggt cct cct cgc atc gga ggg aag cgt gaa ctg 163
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
 10 15 20
 aag ttc ggg ctg gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
 25 30 35
 ctt ggg cag aac ggc cgc caa tgg gtc aac act gga tgg gat tct ttg 259
 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
 40 45 50
 tct gga tgg gat tcc att cag tcc gaa gga cgt tcc taa taa gaa gaa 307
 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
 55 60 65
 atg ctg gat aac ggc gct att tgg ggt gta ctg cag gag cgt ttt gat 355
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
 70 75 80 85
 gac atc gct gat cat gaa aac gat ggt ctg caa ctg tgg att gaa cgc 403
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
 90 95 100
 taa ttc ggc gct gct ggt ggt act gag aac ctg cct gaa cag gaa atg 451
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Glu Ala Met
 105 110 115
 aac aag tgg ttt gat acc aac taa caa taa ctg gty cag gag ttg tct 499
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
 120 125 130
 gag gat aca cgt ttc gtt tgg gat ggc tcc ggc ctg att gag gat ctg 547
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
 135 140 145
 cgt tgc cag cag ggt cgt ggc gtt aat ggc cgc cct gtt ctg gtt ggt 595
 Arg Cys Glu Glu Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
 150 155 160 165
 caa ctg act ttc ctt tcc ctt gct cgc aac act gat ggt tcc aat cct 643
 Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
 170 175 180
 ttg gat caa ctg cct gaa ctg ttt gag gtc taa gag cgc ctg atc aag 691
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
 185 190 195
 tct ttc gat act gag tgg gtt cag atc gat gag cct ggc ttg gtc acc 739
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
 200 205 210
 gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt taa aac act 787
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tot ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gag ctg aac act att gag ggc atc ggc ctt ggc gag att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct ggc tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg att gag ggc atc gtt gat ggt cgt aac att tgg cgt	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gag ctg tct gct gct att gct tcc ctg aag cgc ctg gca gct cgt	1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tot acc tot tgt tca ctg ctg cca gtt cat taa	1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
act ctg gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gct	1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
ttc ggc ccg gag aag atc acc gag ttc aag ctg ctt ggc gac ggc cta	1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
cca ggc aac atc gaa ggc ggt ggc ttc gat ggc ggc tcc gca gca att	1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
ggt tct cga cgc acc tcc cca cgc acc gca cca atc acc cag gaa ctt	1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt aac cgt gca tcc ttc gac act cgt gtt acc ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc	1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat	1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp	
440 445 450	
ctg gtc atc ggc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac	1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His	
455 460 465	

ggt	gag	cca	gag	ggc	aac	gac	atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc	1555
Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	Phe	Ser	Glu	Leu	Leu	
476					475				430						485	
gac	ggt	ttc	ctc	cca	acc	goc	aac	ggc	tgg	gtc	caa	agc	tac	ggc	tcc	1603
Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	
			490					495					500			
ggc	tgt	gat	ggt	cat	cca	ggg	tgg	tcc	gga	aac	gtt	tcc	ggc	cca	ggg	1651
Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn	Val	Ser	Arg	Pro	Ala	
		505					510					515				
cca	atg	act	gtc	aag	tgg	ttc	cag	tac	gca	cag	agc	ctg	acc	cag	aag	1699
Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	Ser	Leu	Thr	Gln	Lys	
		520				525						530				
cat	ttc	aag	gga	atg	ctc	acc	ggt	cca	gtc	acc	atc	ctc	gca	tgg	tcc	1747
His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr	Ile	Leu	Ala	Pro	Ser	
535					540					545						
tcc	ttc	ggc	gat	gat	cag	cag	ctg	gct	acc	act	gct	gac	cag	gtc	gca	1795
Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr	Ala	Asp	Gln	Val	Ala	
550			555					560				565				
ctg	cca	ctg	ggc	gat	gaa	att	aac	gat	tcc	atc	gag	gct	ggc	ggc	aag	1843
Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile	Gln	Ala	Gly	Ala	Lys	
			570					575				580				
att	tcc	cag	ctg	gat	gag	gct	cag	att	ggt	gaa	ctg	tgg	cgg	ctc	cca	1891
Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Leu	Arg	
		585				590						595				
gac	ctc	gat	aag	cat	goc	tac	ctg	caa	tgg	ccc	gtg	gac	tcc	ctc	ggc	1939
Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln	Trp	Ser	Val	Asp	Ser	Phe	Arg	
		600				605						610				
ctg	cag	act	ggc	ggc	gca	ccc	aac	gac	gtc	caa	atc	caa	acc	ccc	atg	1987
Leu	Ala	Thr	Ala	Gly	Ala	Pro	Asp	Asp	Val	Gln	Ile	His	Thr	His	Met	
	615				620						625					
tgt	tac	tcc	gag	tcc	aac	gaa	ctg	atc	tcc	tgg	gtc	atc	ggc	tgg	gat	2035
Cys	Tyr	Ser	Glu	Phe	Asn	Glu	Val	Ile	Ser	Ser	Val	Ile	Ala	Leu	Asp	
630					635					640					645	
goc	cat	gtc	acc	acc	atc	gaa	gca	gca	cgt	tcc	gac	atg	cag	gtc	ctc	2083
Ala	Asp	Val	Thr	Thr	Ile	Gln	Ala	Ala	Arg	Ser	Asp	Met	Gln	Val	Leu	
			650						655					660		
gct	gct	ctg	aaa	tct	tcc	ggc	tcc	gag	ctc	ggc	gtc	gga	cat	ggt	gtg	2131
Ala	Ala	Leu	Lys	Ser	Ser	Gly	Phe	Glu	Leu	Gly	Val	Gly	Pro	Gly	Val	
		665				670						675				
tgg	gat	atc	caa	tcc	cgg	ggc	att	cat	tcc	ggc	cag	aaa	gtg	gac	ggc	2179
Trp	Asp	Ile	His	Ser	Pro	Arg	Val	Pro	Ser	Ala	Gln	Lys	Val	Asp	Gly	
		680				685						690				
ctc	ctc	gag	gct	gca	ctg	cag	tcc	gtg	gat	cat	ggc	cag	ctg	tgg	gtc	2227
Leu	Leu	Gln	Ala	Ala	Leu	Gln	Ser	Val	Asp	Pro	Arg	Gln	Leu	Trp	Val	
	695				700							705				
aac	cca	gac	tgt	ggt	ctg	aag	acc	cgt	gga	tgg	cca	gaa	gtg	gaa	gct	2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323
Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac 2358
Gly Ala Thr Ile
745

00100 104

00110 745

00120 PRT

00130 Corynebacterium glutamicum

00000 104

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr

225	330	235	240
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly	275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Ile Pro Glu Val	325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Ile Val Lys Leu	340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala	355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Asn Ser Ala Arg Ala	425	430	435
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met	435	440	445
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu	450	455	460
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr	465	470	475
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val	485	490	495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn	500	505	510
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln	515	520	525
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr	530	535	540
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr	545	550	555
			560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
555 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
595 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
610 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
625 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
705 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile
740 745

0210 - 10

0211 - 1913

0212 - DNA

0213 - *Corynebacterium glutamicum*

0220 -

0221 - GDS

0222 - (141)...(1900)

0223 - FEMX02085

0300 - 105

gaccgggtga tttegogaac cttgaaacat cgtcagaaga ttgcctgtgg tctagccgg 60

gctgcgcag ttgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa cgt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tgc gat tct ttg Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu 40 45 50			259
tct gga ttg gat tcc gtt cag ttt gca gga cgt tcc tac tac gac gca Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala 55 60 65			307
atg ctg gat acc gcc gct att ttg ggt gtc ctg cag gag cgt ttt gat Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp 70 75 80 85			355
cac atc gct gat cat gaa aac gat ggt ctg cca ctg tgg att gac cgt Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg 90 95 100			403
tac ttt ggc gct gat cgc ggt aac gac acc ctg cat gca cag gac atc Tyr Phe Gly Ala Ala Arg Gly Thr Gln Thr Leu Pro Ala Gln Ala Met 105 110 115			451
acc aag tgg ttt gat acc aac tac caa tac ctg gtc cag gag ttg tct Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser 120 125 130			499
cag gat aac cgt ttc gtt ttg gat ggc tcc gcc ctg att gag gat gtc Ala Asp Thr Arg Pro Val Leu Asp Ala Ser Ala Leu Ile Gln Asp Leu 135 140 145			547
agt tgc cag cag gtt cgt ggc gtt aac gcc cgc cat gtt ctg gtt ggt Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly 150 155 160 165			595
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro 170 175 180			643
tgc gat cag ctg cat gcc ctg ttt gag gtc tac gag cgc ctg atc aac Leu Asp His Leu Pro Ala Leu Phe Gln Val Tyr Gln Arg Leu Ile Lys 185 190 195			691
tct ttc gat act gag tgg gtt cag atc gat gag cat gcc ttg gtc acc Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Gln Pro Ala Leu Val Thr 200 205 210			739
gat gtt gct cct gag gtt ttc gag cag gtc cgc gct ggt tac acc act Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr 215 220 225			787
ttg gct aag cgc gat gcc gtc ttt gtc aac act tac ttc gcc tct gcc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly 230 235 240 245			835
gat cag gcc ctg aac act ctt gcc ggc atc gcc ctt gcc gcc att gcc Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly 250 255 260			883
gtt gac ttg gtc acc cat gcc gtc act gag ctt gct gcc ttg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly 265 270 275			931

gag gag ctg ctg gtt ggg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gag ctg tgt gat gat ctt gct tcc ctg aag cgc ctg gca gct cgc	1017
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
290 300 305	
ggc cca atc gga gtg tct acc tct tgt tca ctg ctg cac gtt cct taa	1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ctg gag gct gag aac att gag cct gag gtc cgc gag tgg ctt ggc	1113
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
tcc gcc tgg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta	1171
Pro Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
gct gcc aac atc gac ccg gct ggc tcc gat ccg ggc tcc gca gca att	1209
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
gct tct cga cgc acc tct cca cgc acc gca cca atc aag cag gaa ctc	1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Glu Glu Leu	
375 380 385	
ccg gct ccg agc cgt cga tct tcc gac act cgt gtt aag ctg cag gac	1325
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Glu Glu	
390 395 400 405	
aac tcc ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc	1383
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca ccg acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1441
Pro Glu Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc atc act ttg gag cag tcc gaa gag gca atg cgc gaa gaa atc gat	1499
Ser Ile Thr Leu Glu Glu Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp	
440 445 450	
ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat ggc ttg gct cac	1507
Leu Val Ile Ala Lys Glu Glu Glu Leu Gly Leu Asp Val Leu Val His	
455 460 465	
ggt gag cca gag cgc aac gac atg gtt cag taa ttc tct gaa ctt ctc	1555
Gly Glu Pro Glu Arg Asn Asp Met Val Glu Tyr Phe Ser Glu Leu Leu	
470 475 480 485 490	
gac ggt ttc ctg tca acc gcc aac ggc tgg gtc caa agc taa ggc tcc	1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser	
495 500 505	
cgc tct gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca ggc	1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala	
505 510 515	

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gca ctg ccg gat gaa att aac gat ctc atc gag gct ggc ggc aag 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

atc atc cag gtc gat gag cct gag att cgt gaa ctg tgg ccc gct aag 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
 585 590 595

aga cgt cca caagcctgcc taactgcagt ggt 1923
 Arg Arg Arg
 600

<210> 106

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<410> 106

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
 1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 21 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 51 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 66 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 101 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Gln Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Ser Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu Glu Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val

485	490	495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn 501 505 510		
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln 515 520 525		
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr 530 535 540		
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr 545 550 555 560		
Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Gln Ile Asn Asp Leu Ile 565 570 575		
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu 580 585 590		
Leu Leu Pro Ala Thr Arg Arg Arg 595 600		

<110> 107

<111> 603

<112> DNA

<113> Corynebacterium glutamicum

<120>

<121> CDS

<122> (111)...(161)

<123> FRXA12156

<400> 107

```

atgatacaga cagatggctac caatgctgac caggttgcac ttgcaatggc agatgaatt 60
aacgatctca tggaggtctg cagaagatc atcaggtgg atg agc ctg cga ttc 115
Met Ser Leu Arg Phe
1 1

gag aac tct tga cag cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

cag tac gag gac tcc ttc cgc ctg gag act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc caa acc caa atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

ccc tgg gtc atc gag ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc gcc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

```

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
 93 95 100

tcc ggc cag aaa gtg gag ggt ctc ctc gag gct gca ctg cag tcc gtg 451
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
 105 110 115

gat cct cgc cag ctg tgg gtc aac cca gag tgt ggt ctg aag acc cct 499
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
 120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtc ctc gtt gag tcc gct 547
 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
 135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgcagg 600
 Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 155 160

aaa 603

<210> 103

<211> 160

<212> 3RT

<213> Corynebacterium glutamicum

<214> 103

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
 1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
 20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
 35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 109

0211- 1326
 0212- DNA
 0213- Corynebacterium glutamicum

0220-
 0221- CDS
 0222- (101)..(1303)
 0223- EXN02645

0400- 109

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa abgcgggttag agtcgaatga 60

aaqtltgata cttctctttcog acttttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5

acc agg acc aac cag gtt ggt tcc ttg ccc cgt acc cca gag cta att 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20

cat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35

ctc caa att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50

aac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cag gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65

acc cgt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gag cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

aca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac ccc gca ttg ttc agc gaa gca tac gag gat cca gca tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acc gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca ggc gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691

Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
			185					190					195			
act	cat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gag	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
		200					205					210				
tac	cag	atc	atc	acc	gat	gca	ggt	ctg	acc	gtt	cag	ctc	gac	gca	cag	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
	215					220					225					
gac	tig	gca	gaa	gca	tgg	gat	cag	atc	aac	cga	gag	cga	agg	gtg	aag	835
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys	
230					235					240					245	
gat	tac	tig	gac	tgg	atc	ggt	aca	egg	atc	gat	goc	atc	aac	agt	gca	863
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala	
			250					255						260		
gtg	cag	ggc	ctt	cga	aag	gaa	cag	acc	egg	ctg	cac	atc	tgc	tgg	ggc	931
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly	
		265						270					275			
tat	tgg	cac	gga	cga	cac	gtc	act	gac	atc	cga	ttc	ggt	gac	atc	att	979
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile	
	280						285					290				
gat	cag	atc	ctc	cgt	gca	gag	gtc	ggt	ggc	ttc	tcc	ttc	gaa	ggc	gca	1027
Gly	His	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala	
	295					300					305					
tat	cat	cgt	cac	gca	cac	gag	tgg	cgt	gtc	tgg	gaa	gaa	aac	aag	ctt	1075
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu	
310					315					320					325	
act	cac	ggc	tct	gtt	atc	tac	cct	ggt	gtt	gtg	tct	cac	tcc	atc	aac	1123
Pro	His	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	Ser	Ile	Asn	
			330					335						340		
gat	tig	gag	cac	cga	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	cag	tcc	goc	1171
Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val	Gln	Phe	Ala	
			345					350					355			
cag	ctt	gtt	ggc	cct	gag	aac	gtc	att	ggc	tcc	act	gac	tgt	ggc	ctg	1219
Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp	Cys	Gly	Leu	
		360					365					370				
gtc	gga	cgt	ctg	cat	tcc	cag	atc	gca	tgg	gca	aag	ctg	gag	tcc	cta	1267
Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala	Lys	Leu	Glu	Ser	Leu	
	375					380					385					
gtc	gag	ggc	gct	cgc	att	gca	tca	aag	gaa	ctg	ttc	taagctagac				1313
Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu	Phe					
390					395					400						
aacgagggtt	gct															1326

C110 - 110

C111 - 401

C112 - PRT

<213> Corynebacterium glutamicum

<400> 111

```

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1          5          10          15

Phe Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20          25          30

Gly Glu Glu Glu Phe Phe Glu Ile Leu Gln Ser Ser Val Asp Asp Val
 35          40          45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50          55          60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Pro Asn
 65          70          75          80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85          90          95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100          105          110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
115          120          125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
130          135          140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Glu
145          150          155          160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
165          170          175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
180          185          190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
195          200          205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
210          215          220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
225          230          235          240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
245          250          255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
260          265          270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
275          280          285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
290          295          300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp

```


Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

cag ttc gcc aag att gtt ggc cct gag aac gtc att ggc tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

cgt ggt ctg gcc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

gag tcc cta gta gag gcc ggt cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

taagctagac aacgagggtt gct 548

<10> 112

<11> 175

<12> PRT

<13> Corynebacterium glutamicum

<400> 112

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 112

<211> 784

<212> DNA

0213 - Corynebacterium glutamicum

0220 -

0211 - CDS

0212 - (101)..(784)

0213 - FRXA02658

0100 - 113

atgaataaaa ttccgggtgc agtgacogta ggtgaggtaa acgcgggttag agtcgaatga 60

gaatttgata ctctcttctcg acttatttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 165
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

cat cca aac atc aac cgt tcc aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc tag att ctg cag tcc tcc gta gag gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

aac ttg ggt atc gac atc ctg aac gag ggg gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

ttc agt gca gtt gac ttc ggt gca tgg tgg aac tac ttc ttc acc cgc 355
Phe Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Phe Arg
70 75 80 85

ctc agc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Phe Met Thr Asp Phe Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca ttg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Phe Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

agg agc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130

ggc atc ttc acc ggt cgc ggt tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145

cca att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165

ttg aag aag ggc atg aac gca ggc gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180

cca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctc acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

CG10: 114

CG11: F23

CG12: FRT

CG13: *Corynebacterium glutamicum*

CG00: 114

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
 225

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu 150 155 160 165	535
aga aac gat ctg cgg aac cat tac aat ccg cac gat gtg tat ttc ttt Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe 170 175 180	643
gat cct tct ggc cag gtg tgg ggg gat ccg cgt tgg ttg ttc aat Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn 185 190 195	691
gag tgg cag tgg atg tcc acg gtg cgg atg gcc cct ctg gtt aat ggt Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly 200 205 210	739
cct tgg ccg gca att tct cct ggt gtc gtc aat cag ctg tcc acg gat Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp 215 220 225	787
gcc tgg ttc gtg ggc tcc aat gat ggc cag tat cag ttc aat ggt tgg Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu 230 235 240 245	835
gga aat ttg gat gat gat ggg cgt ttc cgt tcc gcc ggc cag gcc ggg Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Pro Ala Ala Gln Ala Val 250 255 260	883
tgg acc ttg ggg cat gct gat gtc gca ggc ccc tac aat ttg gtc cct Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala 265 270 275	931
gac ggc ggg cag ttg ctg tgg gag ttc cca acg ctc acc acc gat gac Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp 280 285 290	979
ctc gcc gaa tac aac cca gag gct tac acc aac acc gtc tcc acc ttg Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu 295 300 305	1027
ttt ggg ttg cag gat gga tgg ttg tcc agc gtc agt tcc ggc aat gtg Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val 310 315 320 325	1075
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca ggc Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala 330 335 340	1123
att tcc tcc tcc gcc aat gtg gtg gca ggc gta cgc cac gaa aac aac Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn 345 350 355	1171
gag gca gtg ctt aat gtt ggc tcc atc gaa ggc gtg aat tca gat ggc Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala 360 365 370	1219
ttg agg agt gaa acg atc aat cgt ccc acc ttt gaa tac ggc tgg agt Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser 375 380 385	1267

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc goa cga 1315
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
 391 395 400 405
 tgg gca aca acc ggt gag ctc gtc bag acg gag gcg gag att gtg ctg 1363
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
 410 415 420
 cca agg gat ctg acg ggt ccg atc tct gaa ttc caa ctg tca cga act 1411
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
 425 430 435
 tgg gtc cgg gcc gcc atg att att gaa ggc aag gtg tac gtg ggc gtc 1439
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
 440 445 450
 tta acg ctt cct ggt ccg gcc gag cgg cgc gtc aca aat atc acg gag 1507
 Val Thr Arg Pro Gly Pro Gly Gln Arg Arg Val Thr Asn Ile Thr Glu
 455 460 465
 tta ggg ccg agc ttg cgg gcc ggg ggg ctg tgg atc aac tgg cgc cca 1555
 Val Ala Pro Ser Leu Gly Gln Ala Ala Leu Ser Ile Asn Trp Arg Pro
 470 475 480 485
 tta ggc att ttg ctt ctg gcc acg tca att cca gag acg ccg ctg tgg 1603
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
 490 495 500
 tta ctg gag cag gac cga tca gcc att tgg tgg atg ccg agc ggg aat 1651
 Arg Val Gln Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
 505 510 515
 tta agr gcc ccg gtg ctg gcc gtg gca agt ttc gcc acg arg gtc tac 1699
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
 520 525 530
 tta act gat tgg cat gcc arg ctt cag ctg ccg act gcc gat aat gat 1747
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
 535 540 545
 att tgg cgc cag gtg gcc ggt ttg ctg gcc aag cgt gcc gcc ccg gtg 1795
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
 550 555 560 565
 ttt gcc tac tgatggagct gttcttcacg cgc 1827
 Val Ala Tyr

1100-113

1110-163

1120-PRT

12130-Corynebacterium glutamicum

1400-113

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
 35 40 45
 Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60
 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80
 Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Gln Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Gln Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly

355	360	365
Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe		
370	375	380
Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro		
385	390	395
Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu		
405	410	415
Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe		
420	425	430
Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys		
435	440	445
Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val		
450	455	460
Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser		
465	470	475
Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro		
485	490	495
Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser		
505	505	510
Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser		
515	520	525
Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro		
530	535	540
Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr		
545	550	555
Asp Ala Ala Pro Val Val Ala Tyr		
565		

1310- 119
 1311- 1344
 1312- DNA
 1313- Corynebacterium glutamicum

1310-
 1311- CDS
 1312- (101)..(1311)
 1313- EXA02240

1400- 119
 agatagacc actgacattg cagtttttaga cagtttggtc taatattggt ttttgatttt 60
 agactattt atttctaaact ttttcgaaaag aagggtattt gtc gct cag cca acc 115
 Val Ala Gln Pro Thr
 : :
 gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp

	10	15	20	
aaa ata tgt gat ggt att tcc gat acc att ttg gac ggc ctg ctg gaa				211
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu				
	25	30	35	
aaa gat cag cag tcc cgc gtc gaa gtc gaa act gtc gtc acc acc gga				259
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly				
	40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc ggt tac gta gag atc				307
Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile				
	55	60	65	
cct caa tta gtc cgc aac aag ctg atc gaa atc gaa ttc aac tcc tct				355
Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser				
	70	75	80	85
gag gtt gga ttc gac gga cgc acc cgt ggc gtc tta gta tcc atc ggt				403
Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly				
	90	95	100	
gag cag tcc cag gaa atc ggt gac ggc gtc gat acc tcc gac gaa gcc				451
Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala				
	105	110	115	
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gaa ggt ggt gtc gac				499
Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp				
	120	125	130	
cag cgc ctg atc tcc ggc tac gcc acc aac gaa acc gaa gag tac atg				547
Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met				
	135	140	145	
cct att cat atc gag ttg ggc cag cga ctg tca cat cgt ctg acc cag				595
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Asn Arg Leu Thr Gln				
	150	155	160	165
gtt cgt aac gag ggc atc gtt cat cag ctg cgt cta gac gga aac acc				643
Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr				
	170	175	180	
cag gtc acc ttc gaa tac gat ggc cag gac cgc cat agc cag ctg gat				691
Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp				
	185	190	195	
acc att gtc atc tcc acc cag cag gac cca gaa gtt gac cgt gaa tgg				739
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp				
	200	205	210	
ttg gaa acc caa ctg cgc gaa cag gtc att gat ttg gta atc aac gac				787
Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp				
	215	220	225	
gaa ggc att gag gat ctg gaa acc ggt gag atc acc gtg ttg atc aac				835
Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn				
	230	235	240	245
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat ggc ggt ctg				883
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu				
	250	255	260	

acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat 931
 Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
 265 270 275

ggt agt gga gga ttc tcc ggt aag gat cca agc aag gtg gac cgc tct 979
 Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser
 280 285 290

ggt gca tac ggc atg ggt tgg gta gca aag aac atc gtg gca gca ggc 1027
 Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
 295 300 305

att ggt gat cgc ggt gaa ggt cag gtt gca tac ggc att gga cgc gca 1075
 Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
 310 315 320 325

gag cca gtc gga att tac ggt gaa acc ttt gac acc aac aag gaa ggc 1123
 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
 330 335 340

gag agc gac gag cag att cag ggt ggc gtc ttg gag gtc ttt gac ctg 1171
 Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu
 345 350 355

att cca gca gca att atc ggt gag att gat cag att ggt cgc atc tac 1219
 Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
 360 365 370

ggt aac act ggt ggc tac ggc cag ttt ggt cgc acc gat ttg gac att 1267
 Ala Asp Thr Ala Ala Tyr Glu His Pro Gly Arg Thr Asp Leu Asp Leu
 375 380 385

att agg gag ggt atc gat ggc ggt gat gaa ctt cgc gca ggc ctc aag 1315
 Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys
 390 395 400 405

ttg acc aaaaaattcg atgtagtacc ctc 1344
 Leu Ala

110-120

111-407

112-BRT

113-Corynebacterium glutamicum

1400-120

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr
 1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu
 20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr
 35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser
 50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65		71		75		80
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val						
		85		90		95
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp						
		100		105		110
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg						
		115		120		125
Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu						
		130		135		140
Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser						
		145		150		155
Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg						
		160		165		170
Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Glu Asp Arg						
		175		180		185
Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu						
		190		195		200
Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp						
		205		210		215
Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile						
		220		225		230
Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met						
		235		240		245
Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly						
		250		255		260
Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser						
		265		270		275
Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn						
		280		285		290
Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Ser Val Ala Tyr						
		295		300		305
Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp						
		310		315		320
Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu						
		325		330		335
Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu						
		340		345		350
Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg						
		355		360		365
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
		370		375		380
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
		385		390		395
						400

Arg Ala Ala Leu Lys Leu Ala
405

<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 121
tcggtatccc gaggtacact taga 24

<210> 122
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 122
ctatcccccgg gcatcgaaac tta 23

<210> 123
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 123
gtatgcaacta tgacccatg 18

<210> 124
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 124
gtataaacgac ggcccatg 17

<210> 125
<211> 4334
<212> DNA
<213> Corynebacterium glutamicum

<400> 125
aaatcgcttg accattgcag gttgggtttat gactgttgag ggagagactg gctcgtggcc 60

gacaatcaat gaagctatgt ctgaatttag cgtgtcacgt cagacccgtga atagagcaact 120
taagtctggg ggcattgaac ttccacgagg accccgtaaa gcttcccagt aaatgtgcca 140
tctcgttagg agaaaaagggt tccccccgta ggggtctctc tcttggccctc cttctctaggt 240
cgggctgatt gctcttgaag ctctctaggg gggctccac ccacaggcaga taacgggttc 300
ccacccgctc acctcgttaag ccacacaagg atgtctccaa agatcttcaa agccactgac 360
ggactccgc ttccggaagg cttgccccgc ggaaatttc ccacccaggt tctgtccac 420
ccctatgcca agctctcttc accttaaaat ccagagattg gattcttacc gtggaaattc 480
ttcgaaaaaa tcttccccg atgcacctg ccacgtctgt ccgggggggt ccgctgggtt 540
cgcttggctt gacccactt atccagcttg atgctgag gtccagggat ccccggggtg 600
gaaagccacg tctgtctca aaatctctga tcttacctt cacaagata aaatatatca 660
ccatgaacaa taaaactgct cgttacata aacagtaata caagggggtg tatgagccat 720
attcaacggg aaactctctg ctccaggcag ccattaaat ccaacatgga tcttgattta 780
tatgggtata aatgggctcg ccataactg gggcaatcag gtccgacaa ctatcgattg 840
tatgggaagg ccagtcgac agactgctt ctgaaactg gcaaaaggtag cgttgcacat 900
gatgttacg atgagatggt ccactcaaa ccgctgaggg aacttatgca tcttccgac 960
atccagcatt ctatccgtac tctgcatgt ccactggtaa ccaactgca jactccgggg 1020
aaaaagcatt tccaggtatt agaaacatat cctgattcag gcaaaatat tcttgatggg 1080
ctggcaggtt tcttgccag gttgcattg attctgtct gtaattgtcc ttttaacagc 1140
gatccgctat ttgctctgc tcaaggcaca tcaagcaatg ataacggctt ggttgagcgg 1200
agtgattctg atgacgagcg taatggctg cctgttgaa aagtctggaa agaaatgcac 1260
aagcttttgc cattctcacc ggattccagt gtcactcat gtgatttctc acctgataac 1320
cttatttttg accaggggga atcaataggt tctattgat tgggaagagt ccggaatgca 1380
gacccgatac aggatcttgc cactctatgg aactgctcg gtagtcttc tcttccatta 1440
cagaaaaggc tttttcaaaa atatggcatt gataatcctg atatgaataa attgcagttt 1500
catttgatgc tggatgagtt ttttaataca gaattggta attggttgta acactggcag 1560
agcattacgc tgaactgac ggacggcggt cttgttgaa aaatcgaaat tttgctgagt 1620
tgaaggatac gatccgcac cttcccgaca acccagaccc ttcctgtgga aagcaaaagt 1680
tcaaaatcac caactggctc acctacaaca aagctctcat caacccgtgg tccctcactt 1740
tctggctgga tcatggggcg attcaggcct ggtatgagtc agcaacacct tcttcacgag 1800
gcagaccca ggcctccga attgatcagt actggcgct cgtgatcgc cctccgcagc 1860
ttgtcgggtt ggttgtctc tgaggcgct gcacagata gctaaaaatc tgcgtcagga 1920

tggcgttaga gggcggtgog ggtcgattgg aggcctcccc tttggttgac ggtcttcaat 1330
cgctctacgg cgaccccgac gctcttttgt tgggtacgt cgatcgtttt attctgtgog 1340
atcccgaaaa agttttcgcc tttgttaaaa aaattctcgg tggcccgga aattttcgat 1350
tcagattttt ttaaaaaaca agccagaaat acgacacac gtttgagat aatctgtctt 1360
tcggaaaaat caagtgggat acaaaatttt tagcacccct gagctggga aagtcgggt 1370
tcgtgaaaat tttcggtgog ggtgattttt cgccaaaaac ttaacgaa gttcggtata 1380
atggtgtcat gaacttcacg acgaagtacc aaaattggcc cgaatcaca gctatggatc 1390
tcctgtgatgt cggcgctggag tcggacggcg tcgatgctgc ggtcgattta aaaaagggtga 1400
tcggattttt ccgagctctc gatacgacgg acggcgccagc atcacgagac tgggccagtg 1410
ccggagcgga cctagaaaat ccggtggggg atcttgagga gctgggtgac gagctgggtg 1420
ctgggcagcg ccaggaggac gacacgtagt ggaggatcga atcagttggc cctactggcg 1430
tggtcgatt cctcccgggc ctgacccggg aggaaggggc gcaaaatatt gctcagatgc 1440
ggtctgtgoc gacgcccggc gggagggggc caacaaaagc caaggccagg agctggaggc 1450
gggtaggctc caaatggggc tggaaagtgc tcccctgagc gaaatttggc ccatggtggt 1460
cacagagctg gaagcgggag cgagaattat ccggatctgt ggcgaggtgc ccgcaggcat 1470
gacaaacatc gtaaatggcg ggtttcggtt ggcggggggc gcccaggagc tgcacgggoc 1480
gcacccactt gcacccgaatc ggacgagcg tcggcggtcg aaaaagcgca caggcgga 1490
gaagcgataa gctgcacgaa tacctgaaaa atgtcgaacg cccgtgagc ggtaatcact 1500
agggcgctcg ctaaccccca gtcacaccca gggagaaaag gctcaaaaat gaacttagcg 1510
gattcacgag acattgacac acgggcctcg aaattctcgg ctgatctgtt cgacacccat 1520
cccagctcg cgtcgcgatc acgtggctcg accagcgag accgcggga attcctcgct 1530
cacctgggca gagaaaattt ccagggcagc aagacccggc attcgccag cgttggtatc 1540
aaagacccgg aacggggaga aacacagccg aagtcacac gagttggttc aaaatcgctt 1550
gcccgggtgc agtatgttgc tctgacgac ggcagcagc cagccgtgct tgtccgtggc 1560
attgatgtgc cgagccacca ggcggcgggg aaaatcgagc acgtaaaccc cgaggtctac 1570
ggatttttgg agcgctgggc acgctgggaa aaagcgccag ctgggatcgg cgtgaatcca 1580
ccgagcgga aatgcagct catctggctc attgacccgg tgtatgcgc agcaggccatg 1590
agcagccga atatgcgct gctggctgca accacggag aaatgacccg cgttttcggc 1600
gctgaccagg ctttttcaca taggtgagc cggcgggcac tgcacgtctc cgacgatccc 1610
accggtacc gctggcatgc ccagcacaat ccgctggatc gcctagctga tcttatggag 1620

gttgctcgca tgatctcagg cacagaaaaa cctaaaaaac gctatgagca ggagttttct 3780
agcggaaggg caagtatoga agcggaaga aaagccactg cggaagcaaa agcacttgcc 3840
acgcttgaag caagcctgcc gagcgccgct gaagcgtctg gagagctgat cgaaggcgct 3900
cgtgtcctcc ggaatgctcc agggcgctgc gcccgctgat agaaggcttt cggccacgct 3960
ttgactgtgg gataccagtt aaaagcggtt ggtgagcgcc taaaagacac caagatcctc 4020
gacgcctacg agcgtgccta caccgtcgct caggcggtcg gacagacgg ccgtgagcct 4080
gatctgcgcg cgatcgctga ccgcacagac atggcgcgac gtgtcgcgcg ctacgtcgct 4140
aaaggccagc cagtcgtccc tctctgtcag acagagacgc agagcagccg agggcgaaaa 4200
gctctggcca ctatgggaag acgtggcggt aaaaaggccg cagaacgctg gaaagaccca 4260
aacagtgagt acccccgagc acagcgagaa aaactagcta agtccagtc accacaagct 4320
aggaaagcta aagg 4384